

HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct
5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit
10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis,
15 carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to
20 activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When
25 a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form
30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthien, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

NO. 224, SEQ. ID. NO. 226, SEQ. ID. NO. 228, SEQ. ID. NO. 230, SEQ. ID.
NO. 232, SEQ. ID. NO. 234, SEQ. ID. NO. 236, SEQ. ID. NO. 238, SEQ. ID.
NO. 240, SEQ. ID. NO. 242, SEQ. ID. NO. 244, SEQ. ID. NO. 246, SEQ. ID. NO.
248, SEQ. ID. NO. 250, SEQ. ID. NO. 252, SEQ. ID. NO. 254, SEQ. ID. NO. 256,
5 SEQ. ID. NO. 258, SEQ. ID. NO. 260, SEQ. ID. NO. 262, SEQ. ID. NO. 264, SEQ.
ID. NO. 266, SEQ. ID. NO. 268, SEQ. ID. NO. 270, SEQ. ID. NO. 272, SEQ. ID.
NO. 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282,
SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID
NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300,
10 SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID
NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318,
SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID
NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336,
SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID
15 NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354,
SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID
NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370 ,SEQ ID NO: 372,
SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID
NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390,
20 SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID
NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408,
SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID
NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426,
SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID
25 NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444,
SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID
NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462,
SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID
NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480,
30 SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID
NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498,
SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID
NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
5 NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
10 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
15 SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
20 NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
25 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
30 SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:
499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ
ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ.
 ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID.
 NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO.
 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287,
 5 SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ.
 ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID.
 NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO.
 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321,
 SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ.
 10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID.
 NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO.
 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355,
 SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ.
 ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO.
 15 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381,
 SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ.
 ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID.
 NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO.
 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415,
 20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ.
 ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID.
 NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO.
 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449,
 SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ.
 25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID.
 NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO.
 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483,
 SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ.
 ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:
 30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and
 SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,
 or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.
NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.
NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
5 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
10 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
15 NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
20 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
25 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
 ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
 NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
 5 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
 SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
 NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
 10 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
 ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
 NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
 SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
 15 ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
 ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
 NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
 20 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
 SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
 NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
 25 SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
 ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
 SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
 30 ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:
 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ
 ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60,
 80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5 Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

 Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

 Figure 3 illustrates the multiple sequence alignment derived for fifty novel
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the
25 AOLFR110 amino acid sequence.

 Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entirety.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A⁺ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP₃, cAMP, cGMP, and Ca²⁺ via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain,” “extracellular domains,” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase “functional effects” in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the
5 determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP,
10 IP₃, or intracellular Ca²⁺), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By “determining the functional effect” in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly
15 under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents,
20 radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP₃); changes in intracellular calcium levels; neurotransmitter release, and the like.

25 “Inhibitors,” “activators,” and “modulators” of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation,
30 inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate
5 and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or
10 absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a
15 relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein
20 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
25 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
30 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or
10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the
15 art.

As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide
20 primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma
25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded
5 form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly
15 encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzner *et al.*, *Nucleic
20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term “plasma membrane translocation domain” or simply “translocation domain” means a polypeptide domain that, when incorporated into the amino terminus
30 of a polypeptide coding sequence, can with great efficiency “chaperone” or “translocate” the hybrid (“fusion”) protein to the cell plasma membrane. For instance, a “translocation domain” may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (*e.g.*, an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

“Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relative efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The “translocation domain,” “ligand-binding domain”, and chimeric receptors compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.,* Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

5 The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can
10 also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the
15 invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues
20 which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or
25 coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin
30 (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60° C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding
25 properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase “selectively associates with” refers to the ability of a nucleic acid to “selectively hybridize” with another as defined above, or the ability of an antibody to “selectively (or specifically) bind to a protein, as defined above.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By “host cell” is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and
5 libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of
10 the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

15 The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or
20 plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.*
25 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand
30 using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y. (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain
25 reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwoh, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of
5 vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be “built into” the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that,
10 when ligated, are “in-frame” with respect to the 7-membrane receptor “donor” coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises
15 substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the “donor” 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the “donor” mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues
20 that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of
25 olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through
30 VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g.,* Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. “Natural” base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term “P” in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be
15 used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in
20 culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked
25 to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g., Kroll, DNA Cell. Biol.* 12:441-53 (1993)).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (*see, e.g.,* Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.,* episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.,* chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.,* chlorosulfuron or Basta) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g.,* Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (*e.g.,* TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and “discover modeling”); <http://bioinfo.weizmann.ac.il/>.

5 The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can
10 include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
20 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another
25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, i.e., which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of OR Polypeptides

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

1. Antibodies to OR family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once OR family member specific antibodies are available, individual OR
15 proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20 **2. Immunological binding assays**

 OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see also Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);
25 *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred “sandwich” assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be made by subtracting out cross-reactive antibodies using other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5 e. **Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

 f. **Labels**

15 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS™) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ³H, ¹²⁵I, ³⁵S, ¹⁴C,
25 or ³²P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecule (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID.
NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID.
NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID.
NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID.
5 NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID.
NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID.
NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID.
NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID.
NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID.
10 NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID.
NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID.
NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID.
NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID.
NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO.
15 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249,
SEQ. ID. NO. 251, SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ.
ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID.
NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO.
275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283,
20 SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ.
ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID.
NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO.
309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317,
SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ.
25 ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID.
NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO.
343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351,
SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ.
ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID.
30 NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO.
377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385,
SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ.
ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID.

NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, or conservatively modified variant thereof.

Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID.
 NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID.
 NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID.
 NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID.
 5 NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID.
 NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID.
 NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID.
 NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID.
 NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.
 10 NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.
 NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.
 NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
 15 ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
 NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
 SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
 20 NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
 ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
 NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
 25 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
 SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
 ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
 30 ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
 NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
 SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.

ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, e.g. the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked
5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises
10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in
15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For
20 example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by
25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the
30 activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP γ S assay may be used. As described above, upon activation of a GPCR, the G α subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP γ ³⁵S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP γ S are added to the assay, and binding of GTP γ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP γ S can be utilized.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (\approx 1 nanosecond) for small molecules (e.g. fluorescein) and large (\approx 100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals
5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody
10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,
15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;
20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,
25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about
30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
10 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
20 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and
conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of
the protein, which encodes the structural information of the protein. At least 10
25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino
acids) are entered into the computer system from computer keyboards, computer
readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM),
information distributed by internet sites, and by RAM. The three-dimensional
30 structural model of the protein is then generated by the interaction of the amino acid
sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the
information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as “energy terms,” and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

10 The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

20 Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, e.g., G α 15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, see, e.g., *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269-277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,
10 increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G α 15/G α 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by
10 measuring changes in intracellular Ca²⁺ levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca²⁺ levels are optionally measured using fluorescent Ca²⁺ indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).
30

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

6. Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezeh, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a “knockout” cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, “gene trap insertion” can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene’s expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce “knockout” human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce “knock-ins” in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F. Modulators

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the
15 representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of
20 each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations
25 of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of
30 said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

EXAMPLES

AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIV AISLD
TYLHTPMYLF LANLSFADISSISNSV PKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLL GTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALHTLLLIQLLFCNHNTLP HFFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGKWKAFSTCGSHLTVVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMPMINPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

ATGAAGACTTTT TAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT
GATATTTCTCCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCCTTTACTGTGTGCCAACTCCAAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
5 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LLDVMFSSVVAPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
10 TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFICDLFQLLTLACTDTHILGL
LVTLNSGMMCVAI FLILIASYTVILCSLKSYSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
15 TGTGGAAAATATTTTCTGCTGTGTTTCTTGTCATGTATGTAGCCACAGTGCTGGAAAATCT
ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTCTTA
CCTTCTTGTCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCCCAAGGTGATTGTAGAC
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCTCTCACTGTGATGGCCTATGACCGCTACGTGGC
20 CATCTGTAAGCCCCTGCATACACGATCATGATGAGTCCACGGGTGTGCTGCCTAATGGTA
GGAGGGGCTTGGGTGGGGGATTTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA
TACCCTTCTGTGGTCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT
25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG
TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTCACCCCATAGAC
AAGGCAATGGCTGTGTCAGACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

30

AOLFR5 sequences:

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTL LANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
35 ETLLFLVATL NESVTIMILTSYLLILTILKMGS AGRHKAFTCASHLTAITVFHGTVLSIYCRP
SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKELRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCTCTCATCTATGGAGTCACGTTGTTAGCC
40 AACCTGGGCATGATTGCACTGATTCAGGTCAGCTCTCGGCTCCACACCCCATGTACTTTT
TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCCTAGGGTGCATGGTGCAATTCTACT
TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT
GTGGCCATCTGTAACCCCTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
45 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCATTGTGCTTAGCTCTT
AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT
AAGTCTTGCTTGTCTGATATCACTGTGAATGAGACACTGCTGTTCTGCTGGTGGCCACTTTG
AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
50 GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCCAGTTCAGGCAATA
GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACTC
TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
HLSLTDFCFSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTFETFMLAAMAYDRFVAVCK
5 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLSCFESTFINNFICDHSVIVSASYSDPYIS
QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTILFLYCVPNP
KTSSLIVTVASVFYTVAIPLMLNPLIYSLRNKDINNMFELKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTCGTCTACACAGTCACTGTA
10 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATTCAAAACCTCCATACAATCATGT
ACTTTTTCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
CTGTTGGAGAACCTGGTGTGGAATACAGAACCATCTCTTTCTCTGGTTGCATCATGCAAT
TTGTTTTGCTTGCATTTTTGGAGTGACAGAAACTTTCATGTTAGCAGCGATGGCTTATGAC
CGTTTTGTGGCAGTTTTGTAAACCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
20 TGACAGCCATCACTATCTTCCATGGAATATCCTTTTCTTTACTGTGTTCTTAATCCTAAA
ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLNVNLFSETKVISY
VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
FRVLLMSRSLSCASHIHKHFFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIIFSILRIMV
30 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSHIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
PFIYSLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTA
CATCTCTCCCACTGCTTCTCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
35 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCTCAGCTGCAG
AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
TGTCTTTTATGGATATCTGCTTACAAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
CTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
GCTCTGACACATCCTCCAGCCAGATGGTGGTGTGACTGAGACCTTAGCTGTCAATTGTGAC
45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT
CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCTCACTGCAGTAGCCCT
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTAAGTCACTGAGTGGT
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCTTTCTATCTACAG
CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
50 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
LSFIDLCYSSVITPKMLNVNFPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMYFKPPSS
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCCTTGAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTACCCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTTCATTGATCTCTGCTACTCCTCTGTGCATTACCCCTAAGATGCTG
GTGAACTTTGTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
CTTCCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
10 GTTGCTATCTGTGCGCCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCATTCTGTAGGTCTCATAACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTTATTATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT
15 TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTCATGTATTTCAAGCCCCCTTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQFFFFLFLVIYIVTMVGNLGLITLFGNLNSHLHTPMYYFLFN
LSFIDL CYSSVFTPKMLMNFVSKKNIISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV
25 NEVVVLIVVGTNITVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
SSGSMEQGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCCTAGTGATCTACATTGTCAACCATGGTAGGC
30 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACCTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
35 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC
AGCTTTCTCCTGCACACGACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTCAATTGTCACTAGCATTCTTC
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC
40 TCTGTCTCTGTTTTTTGGGTGAGCGGCATTTCATGTATATTAATATTCTTCTGGATCTATGG
AGCAGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCTCATC
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFNL
SFIDL CYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLRLTFCSANIINHLYCDILPLLQLSCTSTYVN
EVVVLIVVGINIMVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
50 SGSMEQGVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTTTCTGTTCCTAGTGATCTACATTGTCAACCATGGTAGGC
AACCTTGGCTTGATCAATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
55 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACCTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

TTCTCTTTTTTGTGCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
GCCATCTGTAATCCATTGCTGTATAAGGTGACCATGTCCCATCAGGTCTGTTCTATGCTCAC
TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
5 GCTTTCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
ATCATGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTTCATTGTCACTAGCATTCTTCA
TATCAAAATCCACTCAAGGAAGATCAAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGCT
CTGTCTCTGTTTTTTGGGTCAGCGGCATTTCATGTATATTAAATATTCTTCTGGATCTATGGA
GCAGGGAAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
10 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGA
GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS
15 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFCFVNSECYVLVSMA YDRYVAICNPLLY
MVTMSPRVCFLLMFGSYVVG FAGAMAHTGSMRLRTFCDSNVIDHYLCDVLP LLQLSCTSTHV
SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIIA VALFFGSGTFTYLTTS
FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC
CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT
CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTTACCCCCAAAATGCTGA
ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
25 TGTTCCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTTCTGCTGATGT
TTGGTTCTATGTGGTAGGGTTTGCTGGGGCCATGGCCCACTGGAAGCATGCTGCGACT
GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC
TCTCCTGCACCAGCACCCATGTGAGTGAGCTGGTATTTTTTCATTGTTGTTGGAGTAATCACC
30 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCCACATAATTGCTGTT
GCTCTGTTTTTTGGGTCAGGACATTCACCTACTTAACAACATCTTTTCTGGCTCTATGAA
CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCTTCGATCT
ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
35 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDNCNVLNFF FADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL
LGLSSRPEDQKPLFAVFLPIYLITVIGNLLIILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMAIDRYVAICNPFHYITIMSHRCCVLLL VLS
FCIPHFSLLHILLTNQLIFCASNVIIHFFCDDQPVLKLSCSSHFVKEITVMTEGLAVIMTPFSCIII
SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA
AGAATAAAAAGGAGAAATTTTGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCTCTGA
ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTC
TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
50 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTTGACATTTGCT
ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAACACAGACAGTTAC
CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
CCATTATGAGTCACAGATGCTGTGTCCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
55 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCTCTCTCCCATTTTGTCAAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCTTCAGCTGCTGGAAAGCGTAAA
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA
TGTCTATTTTCAGCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
5 ACCGTACTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTHIVLSHLDPHLHNP MYFFFSNL
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
HYTVVMHPCLYVLMASWSVIGFANSLLQTVLILLTLCGRNKLEHFLCEVPPLKLACVDYT
MNESELFVSVIILLVPVALIIFSQIVRAVVRKISATGQRKVFGTCGSHLTVVSLFYGTAIYAY
LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTTGATCTTCTATATCTTCACTTTGCTGGGG
AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCCTCCATTGCT
25 CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACCTCTTCTTTGTGAGTGTCATTA
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTGAGGGCAGTCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCACCTCACA
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAACCTACTC
30 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA (SEQ ID NO: 26)

AOLFR14 sequences:

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSIAIGPKMLVDLLLPRATIPYTACALQMF
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF
RLSFCRSRKINSFFCDIPPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALD TDKMASVFYTLVIPSLNPLIYSLRNKE
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGC
ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCCTGACCTGCCTGCCTGTCTACCTGG
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA
45 CACCTATGTACTTCTTCTTGCCAACTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTTGCTTGCTGGCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG
CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTT
50 ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGACGTGACACCAGTCTCAATGAACTCCTTCTCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGGCGAGCAGCCTCCAC
CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

5 MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLLKLSCDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLFKAFSTCGSHLTVVSLYYGTVMGTYFR
PLTNYSLKDAVITVMYTAVTPMLNPFYISLRNRMKAALRKLFNKRIS (SEQ ID NO: 29)

10

ATGAGGGAAAATAACCAAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTCCTGTTCAATTAACCCATCACATTGATTGGA
AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTGCGCTTACACAACCCCATGTATTTCT
CCTTGCCAACCTCTCCTTGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG
20 CTGAAGTTATCCTGTTCTGACATCCACTTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCCACCTCACGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGATTTCCGCCCTTTGACCAATTATAGCC
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTCAT
25 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

30 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAVAGNLGMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVQCYLFIALVHVEIYILAVMAFDRYMAICNPLL
YGSRMKS SVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINH FYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTA VTIFYATLFFMYLR
PPSKESVEQGKMVA VFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
AGATTTTCTTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCACTGTTACCTT
40 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC
ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
45 AACCTTTCTTTTCTCTCTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA
AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCCTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIIFLVVYIITMVGNI GMMVLIKVSPQLNNP MYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL
55 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTTGTTTAGTACAGTGTTCCTTCTCAT
TGCTCTTGTCATGTGGAAATTTTATTCTTGTGCGATGGCCTTTGATAGATACATGGCAA
10 TTGGGAATCCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
ACATATCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

20

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFVLFLVVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLA FVDLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFS DGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
25 EHAMFISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAACCTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGATCTGCTTG
35 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCTGACCTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCATTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGTCCCTACCATCGTCTTGGTGTCTATGCCTTCATTCTTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
40 TGTCACCCTGTTTTATGGGACTCTCTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRSLFCASHIHKHFFCDTQPVLKLSGSDTSSSQ
MVVMTETLAVIVTPFLCTIFS YLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFR
50 PLSMYSVMKGRVATVMYTVVTPMLNPFYSLRNKDMKRGLKKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
55 TTTTCTCAGCAACTTGCTTTTCATGGATATCTGCTTCAACAGTCATAGTGCTTAAGATG
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 CTCATGTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTG
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCAATTGTGACCCCCCTTCTGTGTACCATCTTCTCCTACCTGCAATCATCGTCACTG
 TGCTCAGAATCCCTCTGCAGCCGGAAGTGAAGGCCTTCTCTACCTGTGGCTCCACCT
 CACTGTAGTGGTCTGTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 10 ACCCTTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTHPELKTLLFVFFAIYLYLITVVGNI SLVALIFTHCRLHTPMYIFLGN
 15 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPLYRLSCVDPF
 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
 NLLEEGGNDIPAILFTIVVPLLNPFIYSLRNKEVISVLRKILLIKISQGSVNK (SEQ ID NO: 39)
 20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTACACACCAATGTACATC
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTAT
 25 TTTCTTTGCACTGTGGAACTGCAGACTGCTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAATCTGCATTCCATGATTATGTAGGGCTTGTA
 TTTAGGTTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCTTTCATCAATGAAGTGGTCTTATTCATCTTCTCAGGTT
 30 CAGTTCAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA
 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTACAATAGTAGTTCCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 TFIDIIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVLLLVMA YDRYVAICKPLHYLV
 40 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLL
 VVANGGLSCTIAFLLLLSYGVILHSLKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSFYTITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

ATGGAGCCAAGGAAAAAATGTGACTGACTTTGTCCTCTTGGGCTTACACAGAATCCAAAG
 45 GAGCAGAAAGTACTTTTGTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
 GCTCATTGTAGTGACCGTAAGTGTGAGTGTGAGACCTGGGCTACCAATGTCCTTCTTTCTT
 GCTGGCTTAACATTTATAGATATCATTTATTCTTTCATCCATTTCCCCCAGATTGATTTTCA
 CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCAGCTCTTTATCGAGC
 ACCTTTTTTGGTGGGTGAGAGTCTTCTCCTGTTGGTGATGGCCTATGACCGCTATGTGGC
 50 CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTGTGCTG
 GTAGTGTCTGGGTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
 TCCCATTTCTGTGGCCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA
 CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
 GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTGATCCTGCACTCTCTAAAGAAA
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCACATCACTGTGGTTG
 TCTTCTTCTTTGTTCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLLTYXXTVVGNLLIVVDIIASPLGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQGCMGQLFIDHFFGGAEVFLLVVMACDRYVAICKPL
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI
GLTVVVNSGAICMVIFNLLISYGVLSSSLKTYSQEKRGKALSTCSSGSTVVVLFVPCIFIYVRP
10 VSNFPTDKFMTVFYTHHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:
43)

ATGAGACANNNNNAACAATATNACAGAATTTGTCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTTCATGTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCCAATGTATTTCTTCCTTG
15 CCTGCCTGTCAATTTATAGATGCTGCATATCCACTACCATTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
ATTTCTTTGGTGGGGCTGAGGTCTTCTCTGGTGGTGTGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACATTTGACCATTGACATCGAATCGACAGGTTTGCTTCCTTCTGTTGG
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTTCAAATTGTTGTGTACAGTCTCCCT
20 TTCTGTGGTCCCNATGTCAATTGTTCAATTTAGTTGTGACATGCACCCATTACTGGAAGTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAAGCTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCTC
TTTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAAGCTTCTACTGATAAGTT
25 CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAAATGCTATAGAAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYSVTIPQILATLATGKTVISYGHCAAQFFLTICAGTECFLLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGA YVCGVSGAILRTTCTFTLSFCKDNQINFFFCDLPLLLKLACSDTA
NIEIVIFFGNFVILANASVILISYLLIKTILKVKSSGGRKTFSTCASHITAVALLFFGALIFMYLQS
GSGKSLEEDKVVSVFYTVVIPMLNPLIYSLRNKDVKD AFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
CCAAATTGGAGATTCCCCTCTTTCTGGTGTTTCTGAGTTTCTACCTAGTCACCCTTCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA
40 GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCAGTTCTTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCACTTGACCT
TCACCCCTCTCCTTCTGTAAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
45 CTGAAGCTTGCCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTTCTATCTGCTCATCATCAAGACCAT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
50 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55 METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITVMGNILIIITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLRRLACTDT

SLLEFLKISNSGLLDVVWFFLLMSYLFILVMLRSHPGEARRKAASCTCTTHIIVVSMIFVPSIYLY
ARFPTPFPMDKLVSIGHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTCTGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTTCTGTTTCTAATGTTCTGTTTGTCTACATCACCCTGTTATGGGA
AACATCCTTATCATCATCACAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
GCTCCGAAACCTGGCTGTCCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAATGCTAG
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
CTTCCACTTTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCCTCA
10 TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
CCACTGCCCTTCTGTGGCCCCAACATTTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
GAGACTTGCCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
CTGGATGTCGCTCTGGTTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
15 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCCGCCCTTCACTCCATTCCCTA
TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA
TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
TTGA (SEQ ID NO: 48)

20

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLNL
LIDFCSTTTITPKMLMSFVSRKNISFTGCMTQLFFFCFFVVSSESFILSAMAYDRYVAICNPLLYT
VTMSCQVCLLLLGA YGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPILLESCNSSYMN
25 ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
LSILPLEQGVSSLFYTHVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

30 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
CCTGGGCTTGATAACCTGATTGGGCTGAACCTCTCACCTGCACACTCCCATGTACTTCTTCC
TTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAATGCTGATG
AGTTTTGTCTCAAGGAAGAACATCATTTTCTTCCAGGGTGTATGACTCAGCTCTTCTTCTT
CTGCTTCTTTGTCTCTCTGAGTCCTTCATCCTGTGAGCGATGGCGTATGACCGCTACGTGG
35 CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTG
TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
CTGACCTTCTGTGCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCTCCTTGA
GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
GTTGGAATGCCATTGTCACTGTCTTTATTCTTATGCCCTCATCCTCTCCAGCATTCTACA
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCACTTCCCACATAATTGTA
40 GTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
GAGCAAGGGAAAGTGTCTCCTGTTCTATACCATAATAGTCCCGTGTTAAACCCATTAA
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
TCTTTCTTAA (SEQ ID NO: 50)

45 **AOLFR27 sequences:**

MPSQNYSISEFNLFGFSAFPQHLLPILFLYLLMFLFTLLGNLLIMATTWIEHRLHTPMYFLCTL
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIIHFFCHVLSLLKLACENKT
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
50 LKPKGLHSMYSDALMATTYTVFTFPLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
51)

ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
55 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTTGTGCACCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

5 AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC
TGTGGATCCCACCTACCATGGTTGGTTTCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTCT
GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

10 MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMIT
LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNIISYAGCMSQLYFFLVFVIAEC
YMLTVMAYDRYVXXCHPLLYNIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY
FCDILPLMKLSCSSTYDVENTVFFSAGFNIIVTSLTVLVSYFILSSILGISTTEGRSKAFSTCSSHL
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAQVQKTLRGK
LF (SEQ ID NO: 57)

15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
GAAATCACTCTACAGTGACAGAGTTTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
AGCTCCCCCTCTTTCTCTCTCCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC
ATGATCACTCTAATTTGTCTGAACCTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACCTTG
20 TGTGAGAGAAAAACATCATCTCCTACGCAAGGTGCATGTCACAGCTCTACTTCTTCTTGT
TTTGTGCTATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
TGCCACCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCTCATGTTAAACTGCCCC
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCCTG
25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC
ACGAGCTTAACAGTTCTTGTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGACGCCGTGGGAAT
GTTCTATGGATCAACTGCATTCATGTACTTAAACCCTCCACAATCAGTTTCTTGACCCAG
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
GA (SEQ ID NO: 58)

AOLFR31 sequences:

35 MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIVLIRSHHLHTPMYIFLCHL
AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLAAMAYDRYVAICSP
LLYSTCMSPGVCILVGMSSYLGGCVNAWTFIGCLLRLSFCGPNKVNHFCDYSPLKLACSHDF
TFEIIPIASSGSIIIVATVCVIAISYIYILITILKMHSTKGRHKAFSTCTSHLTAATLFYGTITFIYVMP
KSSYSTDQNKVSVFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT
AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT
TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
45 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
TGTGGCCATCTGCTACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCATTGGCTGCTTATT
AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACCACTTT
TGAAGCTTGCTTGTTCCTATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
50 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
55 AAAATATTTTCTTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
MSTQVSVQLLL VVYIAGFLIAVS YTTSFYFLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLSF
5 SSGSIIVVTVCVIAVCYIYLITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
DQNKVSVVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNIT (SEQ ID
NO: 61)

ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
10 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCCTATGTATTTCTTCTGAGCCACTT
GGCTTTTGCTGACATGGCCTATTCATCTTCTGTACACCCAACATGCTTGTAACACTTCCTGG
TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCCTTCTATTTTTTACTCTTCT
GTGGACCAAATCAAGTCAATCATTTTTTCTGTGATTTGCTCCCTTACTTGAACCTCTCCTGT
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTTCTTCTGGATCCATCATTGTGGTCAC
TGTGTGTGT CATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
20 CTGAGGGGACCACAAGGCCTTCTCCACCTGCACTTCCCACCTCACTGTGGTTACCCTGTT
CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

AOLFR34 sequences:

MLEGVEHLLLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT
ECFLYTL MAYDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVFRLPFCGPNRV
30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST
CAAHLT VVIVVYPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIYTLCNKEMKAALQRLGG
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
35 AACTGCAAAGTGGAACCAAGACTTCTGTGTCTCACTTCATTTGGTGGGCCTGCACCACCC
ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCTTGTCTATCTCCTCACTGTTTCTG
GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
GTTCTGTGTACCTCTCCTTCTTGGACATGACCATTCTTGTGCTATTGTCCCCAAGATGC
TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTGGGGGCTGTGTAATCCAACATATT
40 TCTTTCCATTCTCTGGGCTGTACTGAGTGCTTCCCTTTACACACTCATGGCTTATGACCGTTT
CCTTGCCATTGTGAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTGTATT
CCGGCTGCCCTTCTGTGGCCCCAATCGGGTTCGACTACATCTTCTGTGACATTCTGCCATGC
TGCGTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTCAGACATTGGCTT
45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCCTATGGCTATATTGTAGCTGCCATCC
TGCGAATTCGTCAGCAGATGGGCGCCGCAATGCCTTCTCCACTTGTGCTGCCACCTCAC
TGTTGTCAATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTACAGGAGC
CCCTGGATGGGGTGGTAGCTGTCTTTTAACTGTCATCACTCCCTTGCTTAACTCCATCATC
TACAACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG
NLSTLDICYTPTFVPLMLVHLLSSRKTSFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL
55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCTCCTGGG
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCCGTGACTTC
TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCCTCTGATGCT
GGTCCACCTCCTGTCTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
10 TGAGCCTGTCCACGGGCTCCACGGAGTGCTGCTACTGGCCATCACGGCCTATGACCGCTA
CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG
CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT
CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTCCTACTTGCTCATCCTGGCCACCA
15 TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTAAGTGAAGCCCAAGAGTAAG
GAAGCCACATCTCTGATGAGGTCTTCACAGTCCTCTATGCCATGGTCACGACCATGCTGA
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

AOLFR36 sequences:

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYYKIVPSILRIS
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAPPLRNGMVASVMYAVVTPMLNPFYIS
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC
ACCCCCACACACCCATGTACTTCTTCTCCTCCTCAACCTGTGCTGGGCTGACATCGGTTTCACC
30 TTGGCCACGGTTCCCAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTTCT
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCCTCTGCACTACCCAGTCATC
GTGAATCCTCACCTCTGTGTCTTCTTCGTTTGGTGCTCTTTTCTTACGCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT
35 TTGCTGTGAGCCATCTCAACTTCTCAAGCTTGCTCTTATGACAGCGTCATCAATAGCATA
TTCATATATTTTGATAATACTATGTTTGGTCTTCTTCCATTTCAGGGATCCTTTTGTCTTAC
TATAAAATTGTCCCTCCATTCTAAGGATTCATCATCAGATGGGAAGTACAAAGCCTTCT
CAGCCTGTGGCTGTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
40 GTGGTCACCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCTTAG
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**

MEKANETSPVMGFVLLRLSAHPELEKTFVLLILLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSFLTQPETISFSACAVQMAISFAMAGTECLLLSMMAFDRYVAICNP
LRYSVIMSKAAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGPVLFISFSYVFHITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
50 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKA AVRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
55 GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC
TTCTTCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCCTAGGAGTCCCGTTCTGTTTCATCTCTTTCTCCTATGTCTTCATCATACCA
CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

15 MYLVTVLRNLLIILAVSSDHLHTPMCFFLSNLCWADIGFTSAMVPMKIVDMQSHSRVISYAGC
LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS
SDRKSKAFTSCGSHLAVVCLFYGTGIGVYLTSVSPPPRNGVVASVMYAVVTPMLNPFYISLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

20 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTCTTTGTCTTTTGCATGTATAGAAGACATGCTCCTG
25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTTCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTCAATAGCATA
TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC
30 GCTAACAATGTCCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCAGCTGGCAGTGTGTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTCAACACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCACCCCCATGCTGAACCCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
35 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLSLGLEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRQLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSP
40 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIIKHVFCDIVPLIKLSCSSTYDEL
LIFVIGGFNMVATSLTIIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

ATGGGTGTAAAAAACCACTCCACAGTGACTGAGTTTCTTCTTTTTCAGGATTAACCTGAACAAG
45 CAGAGCTTCAGCTGCCCCCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCAATTACCCCTAAAATGCT
ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTTT
TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
50 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA
TAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTGTCAATTGGTGGATTT
AACATGGTGGCCACAAGCCTAACAAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCCACCTGACA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTS
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
10 RPSRDALHGVVAVFYTTLTPLFNPVVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCCTACTGACAGCGTTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCCAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSSHILIQFLVFLGLMVITYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTDHTISFVSCIIQSYLYFFLGTTDFLLAVMSLDRLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLLRLSCGDTH
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERKAFSTCASHLTVVVIIYGSSIFLY
35 IRMSEAQSKLLNKGASVLSICIITPLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAACCTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTAATTC
TTCCTGCGGAATTTCTCCTTCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC
TCTACTTCTTTCTAGGCACCACTGACTTCTTCTTCTGGCCGTCATGTCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCCACTGTCTCATGGCC
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
CAGGCTTTCTTTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTCATGCTCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTTCACTTGCGCCTCGCATCTTACA
50 GTGGTGGTCATCATCTATGGCAGTTCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTC
CAAACCTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCA
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

55

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFIGGIKIFLLTVMAYDRYIAISQPL
HYTLIMNQTVCALLMAASWVGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
5 LELLMVSNNGLVTLMCFLVLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
(SEQ ID NO: 79)

10 ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
GGGAGCTTCGGTTTGTCTTCTCACTGTTTCTCTGCTGTGTATTTTATGACTGTAGTGGA
AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTCT
CTTGGGCAATCTTTCTTCTGGAATTTTGTACTCTTCCATCACAGCACCTAGGATGCTGG
TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
15 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA
TTGCCATTTCCCAGCCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTATTGTGATGTGCCTCAGCTGAT
CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG
20 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATAACAAGGCCTTTTCGGACATTCCTCA
TGGACAAGGCCGTCTCTGTGCTATACAAATTGTCACCCCATGCTGAATCCTGCCATCTA
TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
ACCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

25

AOLFR43 sequences:

MQKPQLLVPIIATSNGLVHAAAYFLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQIEFNICLAQMFLIHSAVESAVLLA
MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSCYQHTVTHSFLHQ
30 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV
LVFYVPLIGLSVHRLGGPTSLHVMANTYLLPPVNVNPLVYGAKTKEICSRVLCMFSQGGK
(SEQ ID NO: 81)

35 ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
CAGCATACTTCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT
TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
GACCTAGTCTCTCTCTATACCATGCCCCAAGATGGCCAGTCTTTTCTGATGGCCATCCA
GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCCTTATCCATGCTGTGACGCCGTG
40 GAGTCAGCTGTCCTGCTGGCCATGGCTTTTGACCGCTTGTGGCCATTGACCACCATGTC
GCCATGCTTCTGTGCTGACAGGGGTGACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
GGGGTTTGATTTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCTACTGCCAAACAC
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCCTGTACTGACAC
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCCTCTCGGAGGGCA
GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCATGTGGTT
ATGGCTAATACCTACTTGTGCTACCACTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
50 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFGNCIVVFIVRTERSLHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAIESTILLAMAFDRYVAICHPL
55 RHA AVLNNVTVAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTVCVSHIGVVLA FYVPLIGLS

VVHRFGNSLHPIVRVVMGDIYLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTCCATGTATGTAGTGGCAATGTTTGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTC
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGTGGCCATGGCCTTTGACCGTTATGTGG
10 CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCTCAACAATACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC
15 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
CTTCATCCCATTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA
MLATIDLVLSSSTLPKMLAIFWFRDQEIFFACLVQMFFLHSFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDT
25 SFNNIYGIAMFVSVLDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

30 TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCTTCTCTTCAATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTCTTTCTTCTACAACGCTGCC
35 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGCTGGCCATGGCCTT
TGACCCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCCTGACTGGGTCCCTC
ATCACCAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT
TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTGTTGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTTCGTGAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
ATCTTTGACAATTCTCTAGTATGATAAGGAAAATGAGGTTTCATTCTCACAGATCTACGA
GTCAAGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
50 TTGTCATAGACTACATCATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

55 MNIKHCGWHMIHTWLNIREDDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTTLLITIQLAS

LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFWDLRISFPACFLQMFIMNSFLTMESECTFMVMA
YDRYVAICHPLRYSIITDQFVARAVVFVIARNAFVSLPVMLSARLRYCAGNIKNICSNLSVS
KLSCDDITFNQLYQFVAGWTLLGSDLILIVISYSFILKVVLRIKAEGAVAKALSTCGSHFILIFFS
TVLLVLVITNLARKRIPDPVILLNLHHLPPALNPVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
ACATCGTGTCTCTGCCTACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
15 TCGATCAGCTTCCCAGCCTGCTTCTCCTCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGCTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAAACTCTCTTGTGATGACATCA
20 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCAGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
TGCTGGTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT
GCTCAACATCCTGCACCACCTCATCCCCCAGCTCTGAACCCATTGTTTATGGTGTGAGA
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLHTPTAFLLVGIPGLEHLHIWISIPFLAYTLALLGNCTLLLIQADAALHEPMYFLA
MLAAIDLVLSSALPKMLAIFWFRDREINFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
30 PLHYTKVLTGSLITKIGMAAVARAVTLMPLPFLLRFCFHYCRGPVIAHCYCEHMAVVRACGD
TSFNNIYGIAVAMFIVVLDLLLVILSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGAAACTGCACCTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCCTCCTCAGCACTGCCAAA
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTGCCTGTCTGGCCCAGA
40 TGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCCTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACAACTGTGGTCATCTCTTCACTCATGCACCGTGTA
GCCCCGCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCATATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
50 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFLPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH
55 PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
RVNVVYGLVLIISAIGLDSLLISFSYLLILKTVLGLTREAAQAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPVYGVKTKEIRQLRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
10 GATGTTTGGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
GACCGCTATGTGGCCATCTGTCAACCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGCAGGGGGGCTGCACTGATGGCACCCCTTCCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
15 CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA
TGTGTGTGCTGTGTTTCATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTC
GCAAGCGGCGTGACTCTCCGCTGCCCCGTCATCTTGCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTTCGACAGCGCATCCTTCGA
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

AOLFR49 sequences:

MLTFHNVCSVPSSFWLGTGIPGLESLSHVLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHCFAVESGIFLAMAFDRYVAIC
NPLRHSMVLTYTVVGRGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGLTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

30 ATGCTCACTTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA
35 ATGTTCCCTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGCCATGGCTTTTGA
TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCTGTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTATGCTTGCCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
40 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTTGCTGTTTCTTCCCTGATTACCG
ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAATTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

AOLFR50 sequences:

MNLSFFSFLKSLIMALSNSSWRLPQPSFVLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFSLMLAAIDLVASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLFCQATIIGHAY
50 CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLVKVPNEARLKAFST
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVHVLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCTGGGCATCCTTACCTCCTTGCTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCCTGTCC
 ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC
 TCCTGGTTTCGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
 GCATTCTCCTCCATGGAGTCAGGGGTA CTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
 5 TTTGTCACCCCCTGCACCATTCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
 GGTGGTGCTGGTGCGGGGATTACTACTCCTCATCCCCCTCCTCATTCTGTTGCGAAAACCTT
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
 TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
 10 GTACCAGGAAATGAGGCCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
 TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCCTCACTCACCCTTTGGTCATCATGTA
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
 TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM
 YIIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSISFSACFTQ
 MFFVHLATAVETGLLLTMAFDTRYVAICKPLHYKRILTPQVMLGMSMAITIRAIJAITPLSWMVS
 HLPFCGSNVVVHSYCEHIALARLACADPVPSSLYSLIGSSLMVGSVDVAFIAASYILILKAVFGLSS
 20 KTAQLKALSTCGSHVGMALYLPGMASIYAAWLQGDVVPPLHTQVLLADLYVIIPATLNPIIY
 GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 25 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 30 CTGCTGCTGACCATTGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 GAATTCTACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCAAAGTCCTGC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAAGTGCAGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 40 CTGGGTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY
 CFLCVLAAVDIVMASSVVPKMVSIFCSGDSISFSACFTQMFFVHLATAVETGLLLTMAFDTRYV
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPFCGSNVVVHSYCKHIALAR
 LACADPVPSSLYSLIGSSLMVGSVDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGMALY
 YLPGMASIYAAWLQGDIVPLHTQVLLADLYVIIPATLNPIIYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTTGTGGGTA
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTAGGAAACACCCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 55 ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 CTTTGTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTTCATGACTCCACTG
AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCTACTGTAA
GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAGCACATGT
GGCTCCCATGTGGGGGTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCCAAGTGTGCTAGCTGACCTGTACGT
GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
10 GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTCATGA (SEQ
ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
15 ICNPLRYTTILNHAIVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGIA RLACA
NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLP SHDAQHKALSTCGSHIGIIL VFYIPAF
SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
ACTGGTTGGAAATGCTGCCCTCATCCTGGTCACTGCCATGGACAATGCTCTTCATGCACCT
ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCTTTGGTGGATGCCTGGCC
25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCCTCGATTCTACTTGCCATGGCCTT
TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCCTCAACCATGCTGTC
ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACATACTGTGAGCAT
ATGGGCATCGCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
CATGCAGTCTTTACATCTTCCATCTCATGATGCCAGCACAAGCTCTGAGTACCTGTGGCT
CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTCCTCACCCACCGC
TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
TGCTCTCTGACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTCGGAGTCGACT
35 TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLVHWTMEKSNNSTLFILLGFSQKNIEVLCFVLFVFCYIAIWMGNLLIMISITCTQ
LIHQPMYFFLNYLSLDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTM
40 AYDRYVAICKPLHYTHMSRQKCNTHIVCCTGGFIHSASQFLLTIFVPCGPNIDHYFCDVYPLL
KLACSNHIMIGLLVIANGLIALVTFVVLVLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF
APALFIYIRPVTTFSEDKVFAFYTHAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

45 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTTGTTTTGCTACATTGCTATTGGATGGGAACTTACTCATAATGATTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
50 CATTTCTATAATAACTGTATGATACAACTCTTTACCACCCATTTTTTTGGAGGCATAGAGA
TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTGTGGCCCAAATGA
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

5 AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGCCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTTGTGTTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
ID NO: 104)

AOLFR58 sequences:

10 MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCIDLPLLELACTDTHIFGLMVVINS
FICIINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

15 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCCTTGGATGTACCAACTTGTTAA
TGACTATGATACCAAAATTGATCTGAAGCAAATTTTCTTTGTCTTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTCAAGGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTTCTC
20 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCCTGCTTCTCATCTGTCTCATCCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
25 GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCAGATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
30 TATTGTATATACAGCAGCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

35 **AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSYGLCVVIATLGVDISIFILLSYVLIINTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
40 MVHRFGKHLSPIVHILMADIYLLLPVLPNPIVYSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTG
GACTGGAGTATGTTCACTTCTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATTT
45 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA
TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
GTTCTTCATCCACACATTCACATTCCTGGAGTCTCAGTGTTGCTGGCCATGGCCTTTGACC
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC
50 AAAATTGGTTTGGCCTGTTTGTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCAACCAGGAT
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCAT
55 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT

CCTTAACCCTATTGTCTATAGTGTGTCAGAACAAAGCAGATTCGTCTAGGAATTCTCCACAAG
TTTGTCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5 MFLPNDTQFHPSSFLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAVLVAMAYDSYVAICN
PLQYSAILTNKVVSIGLVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGHLAHLSCASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
10 (SEQ ID NO: 109)

ATGTTCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
15 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAACTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTGT
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC
20 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCACACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT
GTGTGTAATCCTTGCCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATTGCTTTGGCC
25 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCAATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

30 MSIINTSYVEITTFVLVGMPPLEYAHIWISIPICSMYLIAILNGTILFIKTEPSLHGPMYYFLSML
AMSDLGLSSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFLPIINLAVVHRFAG
35 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
40 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT
ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTAAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA
GATTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
TGTCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
50 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55 MFYHNKSIHPVTFLLIGPLEDFHWMISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEA EVLLAMAFDRYVAIC

APLHYATILTSVLVVGISMCIIVIRPVLLTLPVYLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI
NGIYGLFVVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
HRFGHQIPGYIHILVANLYLIIPPSLNP IYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCCTCATTGGAATCCCAGG
TCTGGAAGACTTCCACATGTGGATCTCCGGGCCCTTCTGCTCTGTTTACCTTGTGGCTTTGC
TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
CTACTTCCTGGCCATTCTTTCCACTATTGATTTGGCCCTTCTGCAACCTCTGTGCCTCGCA
TGCTGGGTATCTTCTGGTTTGATGCTCACGAGATTAACATATGGAGCTTGTGTGGCCAGAT
10 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT
GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTACTTACACTTCCCATGGTCTATCTTA
TCTACCGCCTACCCTTTGTGTCAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
CATTGCAAAATTGTCCTGTGGAACATTTCGTATCAATGGTATCTATGGGCTTTTGTAGTTT
15 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTTTTCTTACTCATCGATTTGGACAC
CAAATACCAGGTTACATTACATTCTTGTTGCCAATCTCTATTTGATTATCCCACCTCTCT
CAACCCCATCATTTATGGGGTGAGGACAAACAGATTTCGAGAGCGAGTGCTCTATGTTTTT
20 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPGLEYAHIWISIPICSMYLIAILNGTILFIKTEPSLHEPMYYFLSML
AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS
25 ILTTVRVAQIGIVFSFKSMMLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR
HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
30 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTAAAGCATCTTCCTGTTCAATGCTCCTGAAATTCATCCAATGCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA
35 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
40 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

45

AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVLGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSTVLTPACIVKMGLSSVLRALLILPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN
50 HIYGLFVVACTVGVDSLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
HRFGEHLPRVVHLFMSYVYLLVPPLMNP IYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTCTTCTCCTGACGGGCTTCCAAG
55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
TTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCACT
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
 TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCTCTC
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATAACGCCCTCATCCTTCGCAC
 CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
 TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCTATGTGTATCTGCTGGTACCACCCC
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNTQFHPSSFLLLGIPGLEDVHIWIGVPPFFVYLVALLGNTALLFVIQTEQSLHEPM
 YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFFTAMESIVLVAMAFDRI
 AICKPLRYTMILTSKIISLIAGIAVLRSLYMVVPVFLLLRLPFCGHRIIPHTYCEHMGARLACAS
 20 IKVNIRFGLGNISLLLDVILIILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
 THRFGHNIPQYIHILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCTACTGCT
 GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
 25 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTGGAGGC
 TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
 CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA
 GAAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTCC
 30 ACTGGTGTCTCTCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
 GTGAGCACATGGGCATTTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
 CCTTGGCAACATATCTCTCTTGTATGTTATCCTTATTATTCTCTCTATGTACAGGA
 TCCTGTATGCTGTCTTCTGCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
 GGTTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTTTCATTCTTGACACA
 35 TCGTTTTGGCCATAATATCCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG
 TCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG
 TGCTGAGGATTTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
 ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMLMALDHCVAI
 CFPLRYATILTNVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
 VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
 TFFTHHFGGHTIPLHIHIIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCAGTGTGTACCATGTACAGCATTGCTATT
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
 50 ATGCTCTTCCTTGCCCTTCTTCTTCCACAGATGTGCTCATGTGCACCAGCACCTTCCCAAC
 ACTCTCTTCATATTGTGGTTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
 GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
 TAAAGCTGGGTTCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCTCA
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC
 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCAC
 TTCTGTGCCATAGTCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCAATTTGG
 GGGACACACCATTCCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
 5 CCACAATGAACCCTATTGTGTATGGGGTGAAAACAGGCAGGTACGAGAAAGTGTCTTA
 GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVVGNCGLICLISHEEALHRPMYYFLA
 10 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVMLMALDRYVAI
 CYPLRYATILTNPVIAKAGLATFLRNVMLIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
 FKVNAIYGLMVALLIGVFDICCSVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
 FTFTHRFVGHNPNIHIIIVANLYLLPPTMNPVYGVKTKQIQEGVIKFLLDGKVSFTYDK
 (SEQ ID NO: 123)

15 ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCCTG
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
 GTGGGGAAGTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
 ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGCTACCTTGTGCACCATGTTACCTAAT
 20 ATGTCTGCATATCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCGAGA
 TGTTTTGTGTCATATGCTGACAGGGATGGAGTCTGGGGTGTCTCATGCTCATGGCCCTGGA
 CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
 CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATCACTCTCCTC
 25 ACCAAGCGCTGCCCTATTGCCGGGGAACTTCATCCCCACACCTACTGTGACCATATGT
 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
 TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
 CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
 CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTGT
 30 AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA
 AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTLLMTIWLEASLHQPL
 35 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPIFPACFLQMYIMNCFAMESCTFMVMAYDRY
 VAICHPLRYPSTHDFVKAAMFILTRNVMLTLPILSAQLRYCGRNVIENCICANMSVSRISC
 DDVTINHLVYQFAGGWTLGSDLILIFLSYTFILRAVLRLKAEGAVAKALSTCGSHFMLILFFSTIL
 LVFVLTHVAKKKVSPDVPVLLNLVHHVIPAALNPIIYGVRTQEIKQGMQRLLKKGC (SEQ ID
 NO: 125)

40 ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTG
 GCCGTAGGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 45 CCCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCT
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTTCATGGTTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 ATCCTTTTACGACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 50 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTACGACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 55 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFVLDFNMKNVTEVTFLFVLKGFTDNLELQ
TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
5 KVISFLGCVAVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMPINASYVAGI
LHATIHTVATFSLFCGANEIRRVFC DIPLLAISYSDHTNQ LLLFYFVGSIELVTILIVLISYGLIL
LAILKMYS AEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHD MIVSIFYTIVIPLLNPV
IYSLRNKDVKDSMKMF GKNQVINKVYFHTKK (SEQ ID NO: 127)

10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT
CTTTTTGTCATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC
ATGAAGAATGTCAC TGAAGTTACCTTATTTG TACTGAAGGGCTTCACAGACAATCTTGAAC
TGCAGACTATCTTCTTCTTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA
15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCCTCAGTTATTACCCCAAATATGTTAGTAGAT
TTTACGACAAAGAATAAAGTCATTTCACTTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
GTAGTTTGGAAACCACAGAATGCTTCTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
CATCTACAACCTCTCCTGTATTCACTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
AATGCTTCCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGTGATATCCCTCCTCTCCTTGCTA
TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTGATTCTGTTGGCCATTCTGAAGAT
GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTCCAGCTATGCTTCG
25 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCCTCAT
CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

30 MDSTFTGYNLYNLQVKTEM DKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
YLFTLIGNLGLVVLVIEDSWLHNP MYFLSVLSFLDACYSTVVT PKMLVNFLAKNKSISFIGCA
TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASYVAGILHATIHIVA
TFSLSFCGSNEIRHVFC DM PPLLAISCSDHTNQ LLLFYFVGSIEIVTILIVLISCDFILLSILKMHSA
KGRQKAFSTCGSHLTGVTIYHGTILVSYMRPSSSYASDHD IIVSIFYTIVIPKLNPIIYSLRNKEVK
35 KAVKKMLKL VYK (SEQ ID NO: 129)

40 ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA
AGTTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCCTATTTTTACTATTT
TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG
ATTCTGCTCCACAACCCCATGTATTATTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGCGCAAAAAATAAATCCATT
CATTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
CTCTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCCTCTCCTGTATTCACT
45 GAGCATGTCAACCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTTTAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG
GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCCTCATT
TCCTGTGATTTTATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
50 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
AGTTATATGAGACCAAGTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTT
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTTGAAATTGTTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

MGRNRNTNVPDFILTGLSDSEEVQMALFILLLIYLITMLGNVGMILIIRLDLQLHTPMYFFLTH
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPRLY
PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPRK
SYSLGRDQVASVFYTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
TCCTTACTCAGTTGTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAACCTTTA
GCGAACTTACTGACTTCCAACCTATATTTCTTCTCATGGGCTGCTTTGCCAGATGTTCTTTTT
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
TGCATTTCTGCGACTCAAATGTAGTTCGTCACCTTTTTCTGCGACACGTCTCCAATTTTAGCT
CTGTCCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCACCC
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCTGAAA
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
20 TCACCATCTTTTATGGAAGTATGATTTTTACTTATTTAAACCAAGAAAGTCTTATTCTTTG
GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

MAPENFTRVTEFILTVSSCPQLIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVVSRRLLCLLLVSLTYLYGFSTAIVSSYVFSVSYCSSNIINHFCYDNVPLLALSCSDTYLPE
TVVFISAATNVVGSLLIIVLSYFNIVLSILKICSSEGRKKAFTSCASHMMAVTIFYGTLLFMYVQP
30 RSNHSLDTHDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMNTNLCYSFKTM (SEQ ID NO:
133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGTCTATGGGCTGACCATGGCAGG
35 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCCATGTACTTTT
TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCAATTGCCCTAAATGCTG
ATTAACCTTTTAGTAAAGAAAGAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
GGTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
GTGGCTATTTGTAACCCCTCTGCTGTACATGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
40 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA
ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
AAAATATGTTTCATCAGAAGGAAGGAAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
45 CAGTCACAATTTTTTATGGGACATTGCTATTCTATGTATGTGCAGCCCCGAAGTAACCATTC
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

MNHVVKHNHTAVTKVTEFILMGITDNPLQAPLFLFLIYLVTVIGNLGMVILTYLDSKLHTP
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISSELFILSAMAYDRYV
AICKPLLYVIIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVMIMFYGTLLFIYL
55 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRSLTNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
 CACACCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTACTCCACTGT
 5 CATTGCCCCGAAGATGTTAGTAAACTTCATAGTGACAAAAACACAATTTCTTACAATTGG
 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAAACTGTCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
 AGAGAACTTTAACCAATCGATTCAAAATTCCCATTTAA (SEQ ID NO: 136)

AOLFR74 sequences:

20 MEQHNLTTVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 LAFMDLGYSTTVGPKMLVNFVVDKNISYYFCATQLAFLVFIGSELFILSAMSVDLYVAICNPL
 LYTVIMSRRCVQLVAIPYLYCTFISLLVTIKIFTLSCGYNVISHFYCDLPLPLLCNSNTHIELI
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLFLFMYVQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCCTCACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACGTGGGGACCCAAAATG
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
 30 TTTCTTTCTTGTGTTCACTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 ATGTGGCCATCTGTAAACCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCAATTTCTCTTCTAGTCACCATAAAGATTT
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
 35 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCTT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCTGGTTATCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAAAATATGCCCTACGAAGGACATGGAATAACTTATG
 40 TAATATTTTGTTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLLGFWQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMAHLHFCSDNVIHHFFCDINSLPLSCSD
 TSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSASVIFMVVAPVLNPFYSLRNELKGTLLKTLRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTAAACAGGGCTGTTTGA
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 55 CTGTATGATGTTTGCCAATATGGACAATTTCTTCTCACAGTGATGGCATATGACCGTTAC
 GTGGCCATCTGTCAACCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC
ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC
CCTCTGTCTGTTCCGACACCAAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA
TCTTTGTGGTACCTTCAAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
5 AAAGTCCCTTCTGCCCAAGGAAAACCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT
ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACCTGTGTTGAATCCAT
TCATTTACAGTTTAAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
10 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLDSHLHTPMYFFLSNLSLA
GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
VLISSFNVFFALLVTLISYLFILITILKRHTGKGQYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
20 CTACAGGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA
GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG
GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG
25 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
TATAGGCTGTTATGTCAATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTGCC
TCTCTTTCTGCATGTCCAATGTGATTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT
CTTTTTTGCACCTCTTGTACCTTGATTTCCTATCTGTTCATATTGATCACCATTCTTAAGAG
30 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
TTCTTATTTTATAACTGTTCATCATGTACATACGACCAAGTTCCAGTCATTCCATGGA
CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
ATTCTCTAGATTCAGTCTTTTAA (SEQ ID NO: 142)

35

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTMGVAEGVLLVMSYDRYVAVC
QPLQYPVLMRRQVCLLMGSSWVGVNLASIQTSITLHFPYCASRIVDHFFCEVPALLKLSCA
40 DTCA YEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGFLYGA
AVFMYMVP CAYHSPQQDNVVS L F Y S L V T P T L N P L I Y S L R N P E V W M A L V K V L S R A G L R Q M C
(SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
45 CAGGATCACGCCAGTCCTCTTCTCCCTGGTGGCTGTCATGTTTGTATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
TCCTCACACTGATGGGTGTGGCTGAGGGCGTCCTGTTGGTCCTCATGTCTTATGACCGTTA
50 TGTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATACCC
TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCAACACCTGCTCCTCGCACATCA
CGGTAGTGGGGCTCTTTATGGTGCCCGCGTGTTCATGTACATGGTGCCTTGCGCCTACCA

[illegible]

5
10

10

15

30

35

35

40

55

AOLFR80 sequences:

MEGINKTAKMQFFFRPSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
PLRYRLIMSWSLCVELLVGSVLGFLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR
5 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHLVLLQYGCTSFIVLSPS
SSYSPEMGRVVSVAITYFITPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC
CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGATCTGACCAGCCTCGGTGG
10 AAATGCTACAATTGCAGTCATTGTTGAGATCAATCATTCCCTCCACACCCCCATGTACTTTT
TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTTGGCCTTG
GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTCTGCTGGTAGTCATGGCTTATGACCGG
TTTATAGCGATCTGTCAACCCTCTGCGATACAGGCTCATCATGAGCTGGTCCTTGTGTGTGG
15 AGCTGTGGTAGGCTCCTTGGTGCTGGGGTTCTGTTGTCACTGCCACTCACCATTTTAATC
TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCATTCTACTGTGACATGCCTGCAGT
CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
ATCGTCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
20 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCTCCAGTTCCAGCTA
CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
CCCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAAGCATTGAGA
AAATTCTAG (SEQ ID NO: 150)

AOLFR81 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRMSNQTLVTEFILQGFSEHPEYRVFLFSCF
LFLYSGALTGNVLITLAITFNPLGHAPMYFFLLNLATMDIICSSIMPKALASLVSEESSISYGGC
MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
30 TGLMLRLDFCGPNVIIHFFCEVPPLLLSCSSSTYVNGVMIVLADAFYGIVNFLMTIASYGIVSSI
LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
IYTLRNKEVKAAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
ACCGGGTGTCTTATTAGCTGTTTCCTCTTCTCTACTCTGGGGCCCTCACAGGTAATGTC
CTCATCACCTTGGCCATCACGTTCAACCTGGGCTCCACGCTCCTATGTACTTTTCTTACT
CAACTTGGCTACTATGGACATTATCTGCACCTTCCATCATGCCAAGCGCTGGCCAGT
CTGGTGTGCGGAAGAGAGCTCCATCTCCTACGGGGCTGCATGGCCAGCTCTATTTCTCA
40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTGCATGGCCTATGACCGGTACGCAGC
CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC
ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTCTACG
45 GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG
GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCCTCAACCCCT
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTCTTC
50 AGAAATTAA (SEQ ID NO: 152)

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIIISVKASQALKNPMFFFLFYLSL
SDTCLSTSIAPRMIVDALLKKTISFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
55 SQWVCGVLMVAWVGSCVHSLVQIFLALSPLFCGPNVINHCFCDLQPLLKQACSETYVNNLL

VSNSGAICAVSYVMLIFSIVFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTGTTATTTTTTTCGCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTCCTT
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACACTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
10 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTGTG
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA
CAAGCCTGTTTCAGAAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTGCTAATATTCTCCTATGTGCTCTTCTGCAATTCTCTGAGAAAC
15 CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA
TCTTGTTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATCCCCATGGAT
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

20

AOLFR83 sequences:

MGNWTAAVTEFVLLGFSLSREVELLLLVLPTFLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMMSYDRYATICPLRYT
TIMRPSVCIGTVVFSWVGFLSVLFPILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
25 MLSSMVILCCIVLVAYSITYIILTIVRIPSASGRKKAFTNCASHLTIVIIPSGITVFIYVTPSQKEYL
EINKIPLVLSSVVTPLNPFYTLRNDTVQGVLRDVWVRVGVFEKRMRAVLRSLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCCACGTTCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGTCCTGCTCCCGCCTCCACACCCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTCACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATGAGACCTTCTGTCTGCATTGGGACCG
TTGTATTCTCTTGGGTGGGAGGCTTCCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGAGCCCTTGTGGC
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGCG
40 CATTCCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCCACCTGACCATA
GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCCTCAACCCCTTT
ATATATACTCTGAGGAATGACACAGTGACAGGGAGTCCCTCAGGGATGTGTGGGTGAGGGTT
CGAGGAGTTTTTGAAGAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCTCCAACAAA
45 GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

50 MGAKNNVTEFVFLFGLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILIISYVILLNLRQSSED RRKAVSTCGSHVITVLLVLMPPMFM YIRPS
TTLAADKLIILFNIVMPLLNPLIYTLRNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTCTTCCTGA
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
5 ATCTGTAGGCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG
CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
TTAGCATCCTTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
10 GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCCTT
TTGGTTCTCATGCCCCCATGTTTCATGTACATTTCGTCCCTCCACCACCCTGGCTGCTGACAA
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

15

AOLFR86 sequences:

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVFLLIYVTV
GNMLIVVITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC
20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
25 CTCAGTGACCTTGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGCTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
30 GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCTCATTGTTTTCAG
CTCCTCCTGGTCTTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
CTTGTACCTTTTGTGGAAGTTGCCTGCACCAATACGTATGTCAATTGGTCTGCTGGTGGTT
35 GCCAACAGTGGTTTAATCTGCCTGTTGAACTTCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTACTCCTTGAGGTCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
40 TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)

AOLFR87 sequences:

MNNAQLSLGFIDLGIPSVLQKIILTKIILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI
LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIIVVTITTSPLDSPVYFFLSFFSFIDGCSSTMAP
45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVMA YDCYVAICKPLYLITMNRQVCGL
LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCTDTHVFGLFVAANSGLM
CMLIFSILITSYVLILCSQRKALSTCAFHITVVVFFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
LNPLIYTLRNTTEVKNAMKQLWSQIIWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
AGAAAATAATCCTGACCAAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACCTGGATTTCGAGCAAGTGAAC
AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
TTGCTGTGTTTACACTCATCTACTTTCTACCATGGTAGACAACCTAATCATTTGTGGTGACA
55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTTCTGTCTTTCTTTCTTCAT
AGATGGCTGCTCCTCTTCTACCATGGCCCCAAAATGATATTTGACTTACTCACTGAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
 TTGAGATCATTCTGCTCGTGGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
 5 CAATGTCATTGACCATTTTCATCTGTGACCTTTTCCCTCTGCTAAAACTCTCCTGCACTGACA
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
 10 AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 15 LSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFAVVKLVC
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRRDVITQCIQRLQLWLP
 RV (SEQ ID NO: 163)

20 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 25 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTGCATGTCCTATGACCGCTAT
 GTTGCCATCTGTGCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
 TGGCTGTGCATGTGCATGGTTGGGGGCATCCGTGAACTCCCTAATTCACATGGCGATCTTGAT
 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCAGCTGTTG
 30 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
 CCTCCTCCTCCCCATCTCCTGATTTCTACATCCTATGTCTTCACTCCTTCAAAGTGTCACTCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCCACCTCACGGTG
 GTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCATCT
 ATTGCAAGAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCACATTGAATTCTCTG
 35 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
 GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:

40 MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVS
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYL
 CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF
 PFCGPRKVYHFYCEFAVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
 RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
 45 KALRRVLRRDVITQCIQRLQLWLP (SEQ ID NO: 165)

ATGCTGGACCCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
 GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
 50 TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
 ACCCAGCACTTCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTGCATGTC
 CTATGACCGCTATGTTGCCATCTGTGCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
 55 GTGGGACTGATGATGGCTGTGCATGCTGTTGGGGGCATCCGTGAACTCCCTAATTCACA
 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA

5 GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTT
CAAAGTTCATTAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCMDLYPLLELACTDTHIFGLMVVINS
15 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

20 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTTAA
TGAATATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGCTTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTCGGACTTTACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGCTCTTCTGGA
TGCCTGCTTCTCATCTGTCTACCCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTGTGCGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTGCTCTCTCTGAGAACACACAGTTCTGAAGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATGCTGTTGTGATTTTGTGTTTGTGTTTGTGTT
TATTTGTATATACACGACCTCCATCTGCTTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
35 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

40 MGNWSTVTEITLIAFPALLEIRISLFFVLVVTYTLTATGNITIISLIWIDHRLQTPMYFFLSNLSFL
DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLCWVGAFLSVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL
SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLLNPFIYSLRNEKVQEVLRVTRNIMTLIQRKT (SEQ ID NO: 169)

45 ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCTGCAAACTCCAATGTACTTCTTCTCCTCA
GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGTGCTGGTTGCATGATCCAAACATATTTCTACT
50 TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
TATCTGCGACCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTCTTCTGTGACATTGCCCCCTTCTTTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTGCATCCT
55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
CCTCCACCCAGGGCCGTCAGAAAAGCTTTTCTACCTGTGCTTCTCATCACTGTTGTCTCC

ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAAACCTTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE
IWYTTTTPKLLGTFVVARVICMSCLLQAFFHFFVGTTEFLILTIMSFDRLTICNPLHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

10

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCTTGCAAGGCAATGGG
CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATTCCAATGTACTTCTTCCTTTG
TAACCTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCCAGGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCTTCACCACCCACCATCATGACCAGCAAACCTCTGCCTGCAGCTGGCCC
TGAGCTCCTGGGTGGTGGGCTTCACCATTGTCTTTTGTGACACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGA
GCCGCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTA
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

20

25

30

AOLFR93 sequences:

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGH
L SALEILVTTHVPVMLWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
NTLTFEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
VKPKQTQAADYNWVVSMLVSVVTPFLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

35

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTGTCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTCTTCCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG
GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
TGGCTGTCTGTAAACCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
GGTTCTTGTGTCTATGGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
CAAATATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
TGTTGTGATTGGCTACGGCAGCTGCTTGTCTTCTACGTGAAACCCAAGCAAACGCAGGCA
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACCTCTTTCCTCAATCCTTT
CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGTCAACTATTAGGAATTAG (SEQ ID NO: 174)

50

AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSLMDLMLVCTNPVKMAANFLSGRKSISFVGCIGIQLFVCLVGSEGLLLGLMAYDRYVA
ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFCEMLSLLKLAC
5 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
(SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC
10 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
GGGAATGTCTCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT
CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATG
GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG
TCTTCATGCTTCTCTTCCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
20 GTGCTGCAAATGCACTCTGCTCAGGCCTGGA AAAAGGCCCTGGCCACCTGCTCCTCCCACC
TGACAGCTGTCAACCCTCTTCTATGGGGCAGCCATGTTTCATCTACCTGAGGCCTAGGCACTA
CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCCTTACTCCCATGCTC
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

25

AOLFR95 sequences:

MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRLCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
30 RAVDHFYCDRPLQLRLSCSDLFIHRMISFSLSCIILPTIIVIVSYMYIVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCCAGG
CTTCAGGGTACGCCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATTATGCCA
TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
ACCAATGTATTTTTTCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
ACCCAAAGGCTATGATCAACTTCTGCTGAAAACAAGTCTATCTCCTTGCAGGCTGTGTG
40 GCCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTCTCCTGGCGGCCATGGC
TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTCAGACT
AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC
TCGCCCCTTCAGAGACTGTCTTGTCTGATCTCTTTATCCATAGAATGATATCTTTTTCT
45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC
AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLGNFLIVTVTSVDLALQTPMYFFLQN
LSLLEVCFVLVMVPKMLVDLVSPRKHSFVGCQTQMYFFFFFGSSECFLLSMMA YDRFVAICNP
55 LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFCGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTTCCTGGCCATTTATACAGTCACTTTGTTGGGC
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT
10 GGCCATCTGTAACCCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG
CCCTTCTTCTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
AACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
15 AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAGTCC
CCTGAGAGCAAGAAGCTAGTGTCAATTGTCTACACTGTCATCACACCTATGCTAAACCCCA
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

20

AOLFR97 sequences:

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVMVPSFSIAEHWRRMKGANLSQGMFEL
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLKLSFLDFCYSSTVV
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
25 ASLVGSYSAGFLNSLIHTGCIFSLKFCGAHVVTHFFCDGPPLSLSCVDTSLCEILLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
GGAGTTTGAGCTCTTGGGCCTCACCACTGACCCCCAGCTCCAGAGGCTGCTCTTCGTGGTG
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTTCTTGGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAGTGAGTGC
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTGCT
40 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCATTTTTGCTGGTTTCAACCTTTTGAGCTGCACCCTCACCATCTTG
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAATGAGCTCGGCCCAGGGCAGGTTTA
AGGCATTTTCCACCTGTGCATCCCACCTCACTGCCATCTGCCTCTTCTTTGGCACAACACTT
TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
45 TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

AOLFR98 sequences:

MRGFNKTTVVQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEFI
50 LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAMGYDRYVAICHPLR
YTLIINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
LALFSLSILVIMVPFLLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIIYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTTGTGTCATCTTCTCTCCTATACTTGACAATCCTGGTG

GCCAATGTGACCATCATGGCCGTTATTTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTTCATCATCCCTCAGCTGC
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
 CTTTTTCCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
 5 ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATCATAAACAAGGCTGGGGTTGGA
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC
 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
 10 CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAACCACTGCATTGAAAAGAGTTCTTGAATG
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15

AOLFR99 sequences:

MERVNETVVREVIFLGFSSRLRLQQLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
 LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHFFCDIAPVLKLASHHNHFSQIV
 20 IFMLCTLVLAIPLLILVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
 SSSQDALISVSYTHITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
 CCAGGCTGCAGCAGCTGCTCTTGTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
 25 AATGCAATCATCATTTCCACCATTGTCCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
 CCTTGCCATCCTCTCTTGGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
 AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
 30 GTGGCTGTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTC
 CCTGCCTTTTATTCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGCTCA
 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
 CTGGCTATCCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG
 35 TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACCTACTCCTCA
 AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
 TTCCCTGTTGTAA (SEQ ID NO: 186)

40

AOLFR101 sequences:

MDTGNWSQVAEFILGFPHLQGVQIYFLLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
 HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDPFPVLSLACTDTSINV
 45 LVDFVINSCKILATFLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
 KSYSLDYDQALAVVYSVLTPLNPFYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC
 AGGGTGTCCAGATTTATCTCTTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
 AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
 50 TTGTCAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
 GCAAACCTTGCTCAGTGAGAAAAAGACCATTTCACTCTCTGGGTGTCTCCTGCAGATCTATT
 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
 TTAGCCATCTGCCGGCCCCCTCCACTACCAACCCTCATGACCCCAACACTTTGTGCAGAG
 ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGTATT
 55 CACGCCTCCCATTTCTGTGGCCCCAATCGCATTCAGCACGTCTTTGTGACTTCCCTCCTGTG
 CTGAGTTTGGCTTGCATGATACGTCTATAAATGTCTAGTAGATTTTGTATAAATTCCTG

CAAGATCCTAGCCACCTTCCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
TCAGAATTCCTCAGCTGCCGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCTTCCTCAACC
5 CCTTCATCTACAGCTTGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

AOLFR102 sequences:

10 MPVGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIIWVVCTHSTLRTPMYF
FLSNLSFLELCYTTVVVPLMLSNI LGAQKPISLAGCGAQMFFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLFPCGHHQEINHFLCDVPPVLR LACA
DIRVHQAVLYVVSILVLTIPFL LICVS YVFITCAILSIRSAEGRRAAFSTCSFHLTVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

15 ATGCCTGTGGGGAAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT
TCACCACGACCACTGAATTCAGGTTCTTCTCTTCTCTTCTCCTCCTCCTCTACTTGATG
ATCCTCTGTGGCAACACAGCCATCATCTGGTGGTGTGCACACACAGCACCCCTCCGCACCC
CGATGTATTTCTTCTGTCCAACCTGTCTTTCTGGAACCTCTGCTACACCACCGTGGTAGTA
20 CCCTTGATGCTTTCCAACATTTTGGGGGGCCAGAAAGCCCATTTTCGTTGGCTGGATGTGGGG
CCCAAATGTTCTTCTTTGTCACCCCTCGGCAGCACGGACTGTTTCTCTTGGCGATCATGGCC
TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCTCATCATGACCCGCGAGC
TGTGCACGCAGATGCTGGGTGGGGCCCTGGGCCTGGCCCTCTTCCCCTCCCTGCAGCTCAC
CGCCTTAATCTTCAACCCTGCCCTTTTGC GGCCACCACCAGGAAATCAACCACTTCTCTGCG
25 ATGTGCCTCCCGTCTGCGCCTGGCCTGCGCTGACATCCGCGTGCACCAGGCTGTCTCTA
TGTCGTGAGCATCCTCGTGCTGACCATCCCCCTTCTGCTCATCTGCGTCTCCTACGTGTTCA
TCACCTGTGCCATCCTGAGCATCCGTTCTGCCGAGGGCCGCCGCCGGGCCTTCTCCACCTG
CTCCTTCCACCTCACCGTGGTCTCTGCTGCAGTATGGCTGCTGCAGCCTCGTGTACCTGCGTC
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTAC
30 CCCCTTACTCAACCCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

AOLFR103 sequences:

35 MAEMNLT LVTEFLLI AFTEYPEWALPLFLLLLFMYLITVLGNLEMIILILMDHQLHAPMYFLLSH
LAFMDVCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
PLLYVTILTQQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTCGESYT
QEVLIIMFAIFVIPASMVVILVSYLFIIVAIMGIPAGSQA KTFSTCTSHLTAVSLFFGTLIFMYLRG
NSDQSSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

40 ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCT
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCCAGATGCTGG
CAGTGCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
45 GTTCACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
TGGCTGTGTGCCAGCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCCTTGGTGCGGACAGCTCAGCCTTC
ACTCTCTCCTTCTGTGGAACCAAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
50 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCGTGGCCATCAT
GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCCACCTCACTGCT
GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC
GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTCATCCCCATGTTGAATCCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
55 AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
RYNVLMSLRGCTCRVGCWSAGGLVMGMVVTSIAIFHLAFCGHKEIHHFFCHVPPLKLACGDD
5 VLVVAKGVGLVCITALLGCFLILLISYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
VYILPKPGQSPGEDTLMGITYTVLTPFLSPIIFSLRNKELKVMKKTCFTKLFPQNC (SEQ ID
NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
10 CCACCTCCAGCTGATGCTCTTCTCTGCTGTTCCTGCTGATGTACCTGTTACGCTGCTGGGCA
ACCTGTCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGGCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTCACCCACTCCTTCTGCTCACTGTCTATGGGCTACGACCGCTACG
15 TGGCCATCTGCCACCCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
20 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTCGTGCACTATGGCTTTGCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCTCACACCCTTCTCA
GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
CACCAAACCTCTTCCACAGAAGTGTGA (SEQ ID NO: 194)

25

AOLFR106 sequences:

METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNIICTISLDPHLLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQLFFLHFAGASEMFLLTVMADFLYTAICRPLHYA
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
30 ICSSGLISVVCILALLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLTMFGPSIYIYARPD
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
35 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT
GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTCTGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
40 GTGGCTCTCTCCTGGAGGGGGGCTTCATTCACTCTATCATAACAGGTGGCTCTCATTGTTT
GACTTCTCTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGTTCAA
GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTTCCACATT
45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATTA
TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA
TTTTGTGTAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSFILVGILNDSGSPELLCATITILYLLALISNGLLLLAITMEARLHMPMYLLLGQ
LSLMDLLFTSVVTPKALADFLRRENTISFGGICALQMFLALTMGGAEDLLAFMAYDRYVAICH
PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYHPCRAQEIRHLLCEIPHLLKVACAD
TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA
55 ATFMVYLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
(SEQ ID NO: 197)

5 ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATTGGAAGCCCGCTCCACATGCCCATGTACCTC
 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT
 TGCGGACTTTCTGCGCAGAGAAAAACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTCT
 CTGGCACTGACAATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGGCCTAATATATACCGTGTATACC
 10 ATGCACTATCCCTTCTGCAGGGGCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 GACCTTCTGATTCCCTCTCTTGGTGTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGGCCAGTTCCTTCC
 15 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACCTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTGATGCGGGCCTTGAGGAGGGTCCCTGGG
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

20 MCSFFLCQTKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGCTECALLAV
 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSFTFHLPHYWGQNIINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMOSGEGRLKAFSTCGSHLI
 25 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAVTPLNPIIYSLRNKDVKGALRKLVRKRC
 FSHRQ (SEQ ID NO: 199)

ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATATTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 30 TCATTCTCATCTTCTTCTGGATTCTCGCCTTCACTTCCCATGTATTTTTTCTTAGAAATCTCT
 CCTTTGCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACTTCTTGGTA
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAAATTGTCTTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA
 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAAGTCTCT
 35 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTT
 40 CTATGGGTGAGGAATATTCACCTACATGCGACCAAACCTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

45 MLRNGSIVTEFILVGFAQSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
 HSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY
 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 50 PHSTHGPKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

55 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTACGAGAGCTCCA
 CTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAACATATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAACTGCCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT
 5 ATTCCGAGAGCCCTTCCGCAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
 GTGATTGGCCTCTCTTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 10 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLIILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 DASYSFIVAPRMLVDLFSEKKVISYRGCTQLFFLHFLGGEGLLLVVMAFDRIAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL
 LMVFNGLMTLLCFLGLLASAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFIYMCPP
 20 RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO: 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
 25 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTATTGTGGCTCCCAGGATGTTGG
 TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
 CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCCTCATCCTC
 30 CGCTTGCCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTCT
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCTATTA
 TTATACTTCTTATGTTTGGACCTGCTATCTTCTATCTACATGTGCCCTTTCAGGGCCTTACCA
 35 GCTGACAAGATGGTTTCTCTCTTTCACACAGTGATCTTCCATTGATGAATCCTATGATTTA
 TACCCTTCGCAACCAGGAAGTGAAGAACTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 TGTCAGTGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

40 MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLLIYLCALM
 GNVLIIMITTLDDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQQVFLLLSS
 ASAELLLLTVMSFDRYTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLIAMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCSENLIRESIALILINVLDFFCFIVIIITYVHVSTVKKIPSTEGQSKAY
 45 SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMPLPPTFNPIIYSLRNKAIKVALGMLIKG
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
 TTTCTGCGAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTGATTTAT
 50 TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTGGACCATCATCTCC
 ACACCCCCGTGATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTAGTC
 ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCATTTCATTCTTGGCTG
 TGTTTCCCAGGTCTTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
 TGTCTTTGACCGCTATACTGCTATATGTACCCCTCTGCACTATGATGTCATCATGGACAGG
 55 AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT

5 GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAAATTGCACTCA
TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

10 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGIQLPLSLRCLIFSRRKPFLQDASFRPTSS
TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFILITFFFIMISYARIIGAVLKIKTASGRKK
15 AFSTCASHLAVVLIFFGSIHMYVRLKKSYSLTLDRTLAIVYSVLTMPMVNPIIYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

20 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
25 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
30 AGCATTAAAGCACATGTGGCTCCCATTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATAGTGCCCTTGACACCCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAAGTGCAGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTTCATGA (SEQ ID NO: 208)

35

AOLFR114 sequences:

40 MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTTITGNLLIILAIRFNPHLQTPMYFFLSFLS
LTDICFTTSVHPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
HYVTMTSHHCVLLVAFSCSPHLHSLLLTLLNRLTFCDNSVIHHFLCDLSPVLKLSCSSIFVN
EIVQMTEAPIVLVTRFLCIAFSYIRILTTLVKIPSTSGKRKAFSTCGFYLTVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

45 ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
GGCCTGAGGACCAAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
AGGGAACCTGCTCATCATCCTGGCCATTCGCTTCAACCCCATCTTCAGACCCCTATGTATT
TCTTCTTGAGTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
CTGATGAACTTCTGTGCAAAAAGAAGACCATCTCCTATGCTGGGTGTGTGACACAGATGT
ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
CTATGTGGCCGTCTGTGACCCTTTCCACTATGTACCACCATGAGCCACCACCACTGTGTCC
50 TGCTGGTGGCCTTCTCCTGCTCATTTCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCCTTTCTCTGTGACCTCAGCCCTGT
GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTTATATACGAATCCTCACTACAGT
TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
55 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTTCATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5 MEGFYLRSSHQLQGMGKPGRVNQTTVSDFLLLGLSEWPPEEQPLLFGIFLGMVLTVMVGNLLII
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPPLLIVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNRMKEALG
10 KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CCTGTCACTAATGATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACACAGCTATATTTCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCCTCCATTACAGCACATCTATGAGTCCCAGCTCTGTGCACTAATGCTGGGTGT
20 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCACT
GTTCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCTATCTC
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
25 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTCACGCTAAACCCATTCATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTGAGTGGAAAAACA
TTCTTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

30 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCILFLVISWIIHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLILIISYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPFTSHLD
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCCT
40 GCTGGCCAAACCTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
ATGACCTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAACCTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATTCACTCAGTGATTGAGTTGGCTTTTGTGTA
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTAT
CAAACCTGGCTTGATAGACCTACACATTGGGATTGATGTTTACTGCCAATAGTGGATTT
ATTTCTGTGGCTTCTTTTAAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCTCAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
TGGTTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTTCACATCATCTTCTG
50 ATAAATCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSF

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

5

ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCTTCTCATC
10 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
TGTAACAAACAGGTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
CTTGTTGTCTTTGTGGGATCTAAGTTGATATTCACTGGGTTGGTCGTCATCTTTTCTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
20 ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
GCAGTCTCATTCTAATAATTCCCAGGAAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGGAAGGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLGILCMVDMGLATTIIPKILAIFWFDKVISLPECFAQIYAIHFFVGMESGILLCMAFDY
VAICHPLRYPISIVTSSLILKATLFMVLNRNGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTS
30 CDDRRPNISICQLVLAWLGMGSDLSLIILSYILILYSVLRNLNSAEAAKALSTCSSHLTLILFFYTIV
VVISVTHLTEMKATLIPVLLNVLHNIIPSLNPTVYALQTKELRAAFQKVLFALTKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA
35 CTACTGTATCTCTCAGCACTTGCTGCAAACACCCTCATCCTCATCATCTGGCAGAACCC
TTCTTTACAGCAGCCCATGTATATTTTCCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
CCACTACTATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTACCCTCTTCGCTATCCATCAATTG
40 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
ACTCCAGTGCCTGTGCTTGACGACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT
TTGCCAGTTGGTTCTGGCATGGCTTGGGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACCTCAGCTGAAGCTGCAGCCAAGGCC
45 TGAGCACTTGTAGTTCACATCTCACCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

50

AOLFR119 sequences:

MPLFNSLCWFPTIHTVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTLPNALCIFWFSLKEINFNACLAQMFFVHGFTGVESGVLMMLD
RYIAICYPLRYATTLTNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNIISHTYCDHMSVVKL
55 SCASIKVNVYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA

FFTFFAHRFGGHTIPPSLHIIIVANLYLLLPTLNPVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACCTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
10 ATGCTTGCTTGGCCAGATGTTCTTTGTTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCTTTGCGTTATGCTACCACAC
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCCTGAGGGGTGTATTGCTGAT
GATTCCTTTCCCATTTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCATA
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTTGACATTTGTTGTATATCTTTGTCTT
15 ACATTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
TCTTTGCCACCGTTTTGGGGGACACAAATCCCCCTTCTCTTCACATCATTGTGGCTAAT
CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

AOLFR120 sequences:

125 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAHLVVGDLHRLRRPMYF
FLTHLSCLEIWTYSVTPVKMLAGFIGVDGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPIPIYLLSQLTFCGPNVIDHFSCDASPLLALS
25 CSDVTWKETVDFLVSLAVLLASSMVIASVGNIVWTLHIRSAAERWKAFSTCAAHLTVVSLF
YGTLFFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKGALGRVFSLNFWKGQ
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTACCTTG
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAAATATCTCTTATGCTGGTTGCCTAT
35 CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCCTCACACCCATCTTGCCAATCT
ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTCTCCTGTGATGCC
TCACCCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGGAAGGAGACTGTGGATTTCTCTGG
TGTCTCTGGCTGTGCTACTGGCTCCTCTATGGTCATTGCTGTGTCCTATGGCAACATCGTC
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTCACGCCCAT
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
TTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

45

AOLFR121 sequences:

125 MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFVLTLYILTLVANIIVTIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEII
50 NYGVSSSFVIFVPIGLFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLNPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTTAACCTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
 TTTTGTATCTTGGCCACTAATAATTGCTTCCTGCTTACTGCAATGGGGTATGACCGCTATG
 TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT
 GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTT
 5 AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA
 AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCATTTGT
 GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTGCTCTCTCCATCCTTC
 AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
 GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
 10 ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCTG
 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
 ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

15 MEWENQILVEFFLKGHVHPRELLFFVLIFIMYVIVLLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
 YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
 EFLMLVATILFTLMPLLLIVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
 20 KETLNSDDLDATDKIISMIFYGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
 225)

ATGGAATGGGAAAACCAAACCAATTCTGGTGAATTTTTTCTGAAGGGACATTCTGTTACCC
 CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT
 25 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCTTTTCTGGCTGTGCAAGTGCAGATGTTCTT
 GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
 TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
 GGCTGTTGGGTCTGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
 30 CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTCTCATGTGAAATTCTAGCTGTCAT
 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCTCTCATGCTTGTGGCCACAATATTG
 TTCACATTGATGCCACTGCTCTTGATAGTTATCTTACTCATTAAATCATTTCAGCATCCT
 CAAGATTCACCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
 GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
 35 CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
 AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

40 MYRFTDFDVNSIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
 IMYMIILLGNSLLIITILDSRLHTPMYFFLGNLSFLDICYTSSSIPPMLIIFMSERKSISFIGALQM
 VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLQTVLT
 MMLPFCGNNVIDHITCEILALLKLVCSGITINVLIMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
 45 GRKKAFSTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
 GACTGAATTTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTGCT
 50 TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
 CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
 TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
 GTCCTCCTGGCTGTGATGGCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
 55 CCATCATCATGAACGGAGTGCTGTATGTGAAAATGGCTGCATGGTCTGGATCATAGGCTG
 TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTGAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
5 TTTTATGTACATGAAACCCAAGTCAAAGAACTAATAACATCTGATGAGATTATTGGGCTG
TCTTATGGAGTGGTAAGCCCAATGTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)

10 **AOLFR124 sequences:**

MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNLHTPMYVFLTLAVV
DIICCTSHIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHHMCMVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV
15 MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYSPVIYTYIRPASS
YTFERDKVVAALYTLVPTLNPMVYSFQNREMQAGIRKVF AFLKH (SEQ ID NO: 229)

ATGAATCACAGCGTTGTAACCTGAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
AGGGAATTATCTTCCTCTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
20 ATCATCATTGCCAAAATCTATAACAACACCTTGATACGCCCATGTATGTTTTCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
25 ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCCATTGCTGGCTTTG
TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
30 ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCCACATTAAACCCGATGGTG
TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

35 MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEHAI
ISVSVAIGVCYAFSCLVCIVVSVYVYIFSAVLRISQRQRQSKAFSNCVPHLIVTVFLVTGAVAYL
KPGSDAPSILDLLSVFYFVAPPTLNPIYCLKNKDIKSALS KVLWNVRSSGVMKDD (SEQ ID
40 NO: 231)

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
45 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCTCCG
ACATTTGTCCTTCTTAGACCTGTGTCTCATTCTGCCACAGTCCCCAAATCCATCCTCAACT
CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
TCTGTCCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG
50 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
CACTTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTCTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRLTFCNSNIIQHIFYCDII
PLLKISCTDSSINFLMVFI FAGSVQVFTIGTILISYTHLFTILEKKSIKIRKAVSTCGAHL LSVSLY
10 YGPLTFKYLGSAS PQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
ACCGCTCTTCCTGGCATTCTTGGAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
15 TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT
GTAACCACAGAATGTTTTCTCTTGGAACAATGGCATAATGATCGCTATGTAGCCATTTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTCAGCTATTAGTCTTGCA
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTTCAGATTAACTTCTG
TAATTCCAACATAATAACAACACTTTTACTGTGACATTATCCCATTGTTAAAGATTTCTGTGTA
CTGATTCCTCTATTAACCTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTTACCA
TTGGAAC TATTCTTATATCTTATAACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
GATGGAGTCTCTATTTTACACTGTCATAGTTCCTTTATTAAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTACAAAAATGTTCAAAGCAATGTTTAG (SEQ ID
NO: 234)

AOLFR127 sequences:

30 MSNEDMEQDNNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHIFYCDIIPLMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHL LSVSLY YGPLIF
35 MYLRPAS PQADDQDMIDS VFYTHIPLLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATAACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAAAATGCCCTGTTCTTGGTGTCTTGGTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTTCAC
40 ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCAATTTGGTGGAAC TACAGAATGTTTTCTCTTGGCAACAAT
GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCTCCATGCCTTAATTCA
45 TGAAGTCCTTATATTAGATTACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
ATATTATACCACTGTTTATGATTTCTGTACTGACCTTCTATTAATTTCTAATGGTTTTTA
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTACACATTTGCT
CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
50 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATAACAATCATAATTC
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTTCATTACAAA
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55 METQNLTVVTEFILLGLTQSQDAQLLVFVLVLI FYLIHLPGNFLIIFTIKSDPGLTAPLYFFLG NLA
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVM AFDRIYAI CRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNSSLGSLLCFLGLLASYAVILCRIEHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPPQAFP
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

5 ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCACAGGATGTTG
GTGGACTTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
10 TCTTGCAATTTCTTGGAGCGGGAGAGATGTTCCCTCCTCGTTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
CACTTGCCCTTCTGTGGCCCAAACCAGCTCGATAAATTCTTCTGTGATGTTCCACAGGTCAT
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
15 CTCAGCCTCCTGTGCTTCTTGGGCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCATATTATCATT
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCTTCCAGGCTTTCCAGC
TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTCCCTTTGATGAACCCTGTTATTTATA
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
20 CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
25 QIFLLHLLGGVEMVLLVSMADFVVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
AVNLPFCGPNVVDISIFCDLPLVTKLACIDIYFVQVVIVANSGLSFCIILLISYSLILITIKNHSPT
GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTHITPILNPIIYTLRNKEMKISMK
KLWRAFVNSREDT (SEQ ID NO: 239)

30 ATGGCTCTTTATTTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGTC
AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTTTTGGCCTCT
TCTCGGTTATCTATGTGGTCACAGTTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAAC
ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTTGTAGATATGAC
35 CCTTGCTTCTTTTGGCACCCCTAAGGTGATTCTGAACTTGTTAAAAAAGCAGAAGGTAATT
TCTTTTGTCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCCTACACTACATG
ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
TTCCTCAGGGTTTCAGATACCATTGCTGTGAACTTGCCCTTTTGTGGTCCCAATGTGGTA
40 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTTGT
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTTA
TCTCCTACAGTCTGATCCTCATAACCATAAAGAACCCTCTCCTACTGGGCAATCTAAAGC
CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCCTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

AOLFR131 sequences:

MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
50 LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSHIILVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRNHSAGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
KLAVAFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGATGCTTTGTGGTGTTTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCTAAATTCATCATAGAC
TTACTTGCCAAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
5 ATTTGCAAGCCTCTTATTATATGAACATTATCAGTCGTCAACTGTGTCACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACCTCCATAAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCAATTCTGGTCAACTTGAGGAACCAT
10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

15

AOLFR132 sequences:

MVATNNVTEIIFVGFSSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRVISLKGCLTQMPSLHFFGGTEAFLLMVMA YDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLLSVGGTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT
20 FFISLLIITNGGSISVVSFFVLMASYLIILHFLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

20

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCATGGCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGTGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
30 AGGATAGCATGGGGCGGGGGCTGTGCACTTCTGTTGGGCAAACCTTCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGACCACCTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCTGCACTTCTGAGAAG
CCACAACCTGGAGGGGCGAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

40

AOLFR133 sequences:

MTEFIFLVLPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
WQVCTVLVGIAWVGGMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
45 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

45

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
50 ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGGCACTTCTTTGGTGGCACTGA
GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTAAGTGTGCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCTGTCTGTGATCAGTTTGGGGT

55

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
 TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG
 CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
 ACACAGTGATAACCGCGATCCTGAACCCTGTCACTACTCTCTGAGAAATGCTGAAATGAG
 5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
 NO: 246)

AOLFR134 sequences:

MTTIILEVDNHTVTTRFILLGFPTRPAFQLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL
 10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSCE
 DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
 LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQGNAGFS
 S (SEQ ID NO: 247)

15 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
 GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCCTGGCAACCTATCTG
 CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
 AGCCCCATGTACTTCTTGAGCCACCTCTCCTTCCCTGGAGATGTGGTATGTCACAGTCATC
 20 AGCCCCAAGATGCTTGTGACTTCTCCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
 TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
 GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
 AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
 GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
 25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
 CTTCTTGGCCCTCATGGTCATTGCTATTCCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
 TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
 TGCCTCCCACCTGACCGTCGTAATTCTTCTATTCCATGACACTTTTCACCTATGCCCGTC
 CCAAACCTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT
 30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
 ID NO: 248)

AOLFR135 sequences:

35 MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
 AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIIDHFFC
 DAPPLVKMSCTNTRVYEKVLGVVGTFLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
 ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPO
 40 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
 GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
 TCTATTTGGAGTGTCTTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA
 45 TCTTAATCCGAAGTATTCCCCTTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
 TTTTGGATTCTGGTATACCTCTGTGTAATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
 AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTCTGTGTTGTAGCCT
 ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
 ATTGCTTTATTGAGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA
 50 TAGGAGGATTTTGAATGCCATAGCCATACTGCCAATACATTCCGCCTGCATTTTGTGG
 TAAAAATATCATTGACCACTTTTCTGTGATGCACCACCATTGGTAAAAATGTCTGTACA
 AACACCAGGGTCTACGAAAAAGTCCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
 55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTCCACCTACTCCCTAGAGAGGGACAAA
 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVITPKMLVNFLGKKNTILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGFLSALHTSMMKLSFCKSHIINHFCVDLPLLNLSCSNT
HLNELLFIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSSHLMAVVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACACAGCAAG
CAGAGCTCCAGCTGCCCTCTCCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCTTCGTCGATTTCTGCTATTCTCTGTCACTACTCCCAAAATGCTG
15 GTGAACTTCCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTGACTCATACAAGTGCCATGATG
AAACTGTCCTTTTGC AAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCCTCT
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCACTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAGCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

30 MSPENQSSVSEFLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDLHTPMYFFLSH
LALTDISFSSVTPKMLNMNQTHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYRTHIGLYFLP
PSSNTNDKNIIASVIYTA VTPMLNPFIYSLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCGAGTTCTCCTCCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
40 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
TTTTCATATTTTTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT
GTGGCCATCTGTATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTTGTCATGC
TGGTGGCTGGGTCTGGGTATCGCTTGTGCGTGTGCTCTTTGCATACCCTCCTCCTGGCC
CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
45 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAGCCCTTGCCACTTGTGGATCCCACTCTCA
GTGGTGACTATCTATTATCGGACAATATTGGTCTCTATTTTCTTCCCCATCCAGCAACAC
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
50 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTTTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

55 MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTYVIGNPLLY
GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGGGAAT
GGCAAGTTCTCTTCTTCATCGTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTTCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTAGCACAGTGTCTTCTTTCAT
10 TGCTCTTGTCATGTGGAAATTTTTATTCTTGTGCGATTGCCTTTGATAGATACACAGTGA
TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC
TTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTGCCGGCATCAACTTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 256)

20

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILILIIINKEAALHQPMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMADRYVAICRPLRPSIITESFVFKAN
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSDDRRINSINQVLLAWTLMGS
25 DLGLIILSYALILYSVLKLSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
HNVIPPALNPMVYALKNELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

30 ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
35 ACTGAATCTTTTGTTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
TCTCAGTGCCTCTGTTGGCTGCCCAGAGGCATTACTGCTCCCAGAATCAAATTGAGCACTG
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
AACCAGGTCCTTTTGGCTTGGACACTCAAGTGGGAAGTGACCTGGGTTTGATTATTTTATCAT
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAAGCTCTCCAGAAGCTGCATCCAAGGCCTT
AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTACACAGTGCATCATTTGTGATT
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCTTATTCCAGTTCTACTTAATGTGCTACA
CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAACCTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

45 MLTLNKTDLIPASFILNGVPGLEDQLWISFPFCSMYVVMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMMLALDRYV
AICYPLRYSTILNPNVIAKVGATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
FSFFSHRFGHEHIIPPSCHIIIVANIYLLLPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
50 ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
GACTGGAAGACACACAACTCTGGATTTCCCTTCCCATTTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG
55 TACTACTTCTTGGCCATGCTTTCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTGATGAATGCCTTGTCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTCT
 5 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
 TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
 10 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
 CCCACTATGAACCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCTATAA
 GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

MSSTLGHNMESPNTDVEDPSVFFLLGIPGLEQFHLWLSLPVCGLTATIVGNITILVVVATEPVL
 15 HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHFMMESTVLLAM
 AFDYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCFLIGRLNFCQSHVILHTYCEHMA
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
 VILISYTPALFSFFTHRFHHVPHIHILLANVYLLPPALNPVVYGVKTKQIRKRVVRVFQSGQ
 GMGIKASE (SEQ ID NO: 261)

20 ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
 TCTTCTTCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
 25 AACCAGTCTTGCACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
 GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
 CAATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTGGCAGGCTCCCT
 30 GCTCATGCTCCCATGTCCCTTCTTATTGGGCGTTTGAACCTTCTGCCAAAGCCATGTGATCC
 TACACAGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
 ACCGTGTGTATGGGTGACAGCTGCATGTTGGTCACTTGGGTTGACTTGTTTTGCATTGG
 TCTCTCTATGCCCTAAGTGCACAAGCTGTCTTTCGCTCTCATCCCATGAAGCTCGGTCCA
 AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACCAGCCCTC
 35 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
 CAATGTTTATCTGCTTTTGGCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC
 AGATCCGTAAGAGAGTTGTCAGGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
 CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

40 MLGLNGTPFPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 HVNNIYGLLVIIFTYGMDSFILLSYALILRAMLVISQEQRLKALNTCMSHICAVLAFYVPIIAVS
 45 MIHRFWKSAPPVVHVMMNSNVYLFVPPMLNPIIYSVKTKKIRKGILKFFHKSQA (SEQ ID NO:
 263)

50 ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAAACTCCAGCTGACAGGCATTCTCTG
 GGATACAAACAGGCCTCACCTGGGTGCTGCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTGTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCACT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 GCTTTGTGGCTATTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 55 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTACCACCTCTCTTCCCTTTCCCTTTTGTGGT
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCTACGCATTGATCCTGAGAGCC
ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
TCTGTGCAGTGCTGGCCTTTTATGTGCCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
AAAAGTGCTCCACCTGTTGTTTCATGTCTATGTCCAATGTCTACCTGTTTGTACCACCCAT
5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

AOLFR144 sequences:

10 MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFL
SMLSFSDDVAISMATLPTVLRTECLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
PLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
TVHRFGKHVPCYIHVLMNSVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

15 ATGGGGTTGTTCAATGTCACTCACCCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
GAGCTCTCACTCCTGGCTGTCAGGGCCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCATGTACTACT
TCCTGTCCATGTTGTCTTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
20 TATTCACTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCCTTTTCCCTCTTCCCTTTCTTATTAAGA
GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC
25 CTTTGGCATGGACCTGTTTTTATCTTCTCCTCTCCTATGTGCTCATTCTGCGTCTGTGCTATGG
CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
TGTAATTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
GTCCCATGCTACATACATGTCCTCATGTCAAATGTGTACCTATTTGTGCCTCCTGTGCTCAA
CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTCCGCATGTTTCAC
30 CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRLH
TPMYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
35 RFVAICHPLRYSVITGQQVVVRAGLIVIFRGPVATIPVLLLKAFPYCGSVVLSSHFLHQVEVIQLA
CTDITFNLYGLMVVVFVMDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
FVPMMLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIILKLLGLKKASK
(SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
ACCAACCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
45 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTTCATGGAGTC
CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCTCTGAGGTATT
CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
TCTCCCACTCATTTTGCCTGCACCAAGGAGTACAGCTGGCCTGCACAGATACCACCTT
50 CAATAATCTGTATGGACTGATGGTGGTAGTTTTACTGTGATGCTGGACCTGGTGTCTCATC
GCACTGTCCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
ATGGGGCTGTCCCTGGTGCACCGTTTTTGGGAAGCATGCCCCACCTGCTATTTCATCTTCTTAT
GGCCAATGTCTACCTTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
55 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
ID NO: 268)

AOLFR146 sequences:

MSQVTNNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVYFLSM
LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP
5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNCLSHILAVLVLYIPMVGVSM
HRAKHASPLVHVIMANIYLLAPPVMNPPIYSVKNKQIQWGMNLFLSLKNMHSR (SEQ ID NO:
269)

10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
ATGGGCAATACCACCATCTCACTGTCATTCGCACAGAGCCATCTGTCCACCAGCGCATGT
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACTACCCACA
GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAAGTACAGCTCTGAGGCCTGTTTGTCTCAGTT
15 TTTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGCTCCTGGCTATGTCCGTTGACT
GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
AGAAGTGGGTAGCCATCATTGTCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCTT
20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTATTCTGAAAAATA
TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
TCTAGCTGTCCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTAAATTTT
25 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNICILLYLIVVEHSLHEPMF
FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLDSAILMAMAFDHYV
30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
NFWYGFCVPIMTVISDVILIAVSYAHILCAVFGLPSQDACQKALGTCGSHVCVILMFYTPAFFSI
LAHRFGHNVSRFTFIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:
271)

35 ATGCCATCTGCCTCTGCCATGATCATTTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATTCCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCACATTCC
40 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCTGCTGGATTACGCCATTCTG
ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGTGCTGACATGCCTTGCCTTCTGTCAGGACACGCATCATACCCACA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT
ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA
TCTCGCCCATCGCTTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
50 GAGATAAGGTTATACTTTTGTCTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC
MLAGADIVLSTCTIPQALAIWFVFRAGDISLDRCTQLFFIHSTFISEGILLVMAFDHYIAICYPLR
55 YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGR
HIPPCIHIPLANVCILAPPMLNPIIYGKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTCTATCCCATTTCTTCAATTCCTATGTCAACGCCCTT
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCCTCTGCATGTCTGGCTGGAGCAGACATTGTCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
10 ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCTTACAAATGCTCTGATCAA
GAAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGAATAAACATTTGGTATGGGTTTTCCATTCTA
ATGTGCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCTATATGCTGATTCTCCATGC
15 TGTCTTCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTGGGCTCCCATG
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAATCCAGGAACAGGTGGTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

20

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL
SFIDMWFSTVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS
25 AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFQTCASHCIVVLCFFGPGLFIYLR
PGSRKAVDGVVAVFYTVLTPLLNPVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCCTCA
CCAACCTGTCTGTTTATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC
TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT
TTCATTCTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT
35 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACGACACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACATTTCT
ATTTGCCCTACTGTGGACCCAACCTGGATCCAGCACTATTTGTGTGATGCACCGCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGTCTGTCCTATGTGTCCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGAAAGC
TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

45

AOLFR150 sequences:

MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSCMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGDPAFCALHLCLC
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTCTTTCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCATGTACTTCCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACCTGCTCCTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTGACTGCTACA
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG
 10 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
 AGAAAAGGCCATCTCTGTCACCTTCACTGTCTATCTCCCCTCTGCTGAACCCTTTGATCTACA
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMAIDRYVAICSPHY
 SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
 MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFTCASHLTIVTLFYGTLCFMYVRPSE
 KSVEESKITAVFYTLFSPMLNPLIYSLRNTDVLAMQMQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCGATCTACCTAATCACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTT
 25 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 GCACAATTTCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
 CTCTTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 TCACTTATCCTTCTGTGGCTCCCTTGAAATCAATCATTCTACTGCGCTGATCCTCCTCTTA
 30 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 TAATCTCTCAAGCTCTCTCTTCATCATTCTCTGCTCTATCTTTTCATTTTTCAGCGCATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCCTTTCTACGTGTGCTTCCCACCTGACA
 ATAGTCACTTTGTTTTATGGAACCCCTCTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGAGCCCAATGCTGAACCC
 35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
 AAATCCTTTCATAAAATGTCAGTTTAT (SEQ ID NO: 280)

AOLFR152 sequences:

40 MDQINHTNVKEFFLELTRSRELEFFLVVVFVAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
 KSVLDIVFSSITVPKFLVDLLSDRKTISYNDMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
 FALELFMISNGLVTLLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSESARKWG (SEQ ID
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC
 GAGAGCTGGAGTTTTTCTTGTGTTGTGGTCTTCTTGTGCTGTGTATGTAGCAACAGTCCTGGG
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
 50 TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
 GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
 CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC
 TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
 55 GTAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
 TGGTGACCCTGCTCTGGTTCCTCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
GTGGTGACTCTTCACTTCGTGCCTTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
5 CCTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFILTLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
10 RYTSMMSGSRCALLATSTWLSGLHSAVQILTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
NEMVIFVDIGLVASGCFLILVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR
PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:
283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCAATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
20 TCCACTTCTGGGGAGCACCAGAGTGTTCCTCTACACAGTCATGTCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
25 GGCCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCCTTTGCTTTTTTGTNNCCTGTGTTTTCATTTACCTGAGACCAGGCTCCAGGGACGTCG
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIHDNLLIFSAVRL
DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSLNSEGILLTT
35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLILLPEIVMISTLPFCGPNQIQHIFCDLVP
VLSLACTDTSMILIEDVIHAVTHIITFLIILSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
(SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG
45 TGAAGAAGAGGCCATCTCAATGACTGGCTGCATCTTGACAGATGTATTTCTTCCACTCACTT
GAAAACCTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
TGCCTCTTCGGTTTTCTTATCCTGCTTCCCAGAGATTGTGATGATTTCCACACTGCCTTTCTG
TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGATGCTGTGACCATCATCATTACCT
TCCTAATCATTGCCCTGTCCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTTGGACAC
AGCCATTGCACTGATGTTTACTGTACTTGTCTCCATTCTTCAATCCCATCATTTATAGCCTGA
55 GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGTAACA
AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTAVFQFLIGISNYPQWRDFTFFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
5 LRYSVVMNGPVCVCLVATSWGTSVLVTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
NEFMILITSIFTLLLPFGFVLLSYIRIAMAIIRISLQGRLEKAFSTTCGSHLTVVTIFYGSAISMYMKT
QSKSSPDQDKFISVFYGA LTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
10 TCAATGGAGAGACACGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTG
TCCTTGGCTTTGGCCACAGCAGAGTGCCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCCAGTGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
CTTCACCTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCACCC
TGCTGCTACCATTTGGGTTTGTCTCTCTCTACATACGAATTGCTATGGCTATCATAAGG
20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCTCCCC
TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
ACATGA (SEQ ID NO: 288)

25

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPILFMLFLSMYLATMLGNLLIILAVNSDSHLHTPMYFLLSI
LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCELAHILKLACSDVLIN
30 NILVYLVTSLGLGVPLSGIIFS YTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKMDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG
35 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCACCTCCACACCCCATGTACTTCC
TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTCACCTCCACCACGATGCCCAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
TTGTCCTGGTTTTTGTGGATTGGAATGGAATTCTGGTCATGATGGCCTATGATCGATT
TGTTGGCCATCTGTCAACCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
40 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCCTGGATGCTCTGCTGCACACGTTGATGGTGCT
ACAGCTGACCTTCTGCATAGACCTGGAAATTCCTCACTTTTCTGTGAACTAGCTCATATTC
TCAAGCTCGCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTGTTGGTGACCGCT
GTTAGGTGTTGTTCTCTCTCTGCGGATCATTTTCTCTTACACACGAATTGCTCTCCTCTGTCA
TGAAAATTCATCAGCTGGTGGAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
45 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
ACTCATTTACAGCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
GATACCATCTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

MGPRNQTA VSEFLMKVTEDELPKLIPFSLFLSMYLVLTILGNLLILLAVISDSHLHTPMYFLLFN
LSFTDICLTTTTPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHP
RYTVLMNVHFWGLLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMPARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
55 SAVAESSRITAVASVMYTVVPQMMNPFYISLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAAACAGCTGTTTCAGAAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTACAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT
 CTTGTCTTGGTTTTTGGCTGGCTTGGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
 GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACAGGTC
 10 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTATTCTCAAATAGTCACCTCTGTTT
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTTTCCTTGTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAG
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLSFLSMYLVITLGNLLILL
 20 AVISDSHLHTPMYFFLSNLSFLDICLSTTTPKMLVNIQAQNRSTYSGLTQICFVLFFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLLLSLLTSVNVNALLLSLMVLRSLFCTDLEIPLFF
 CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGHLSYQITSCVLRMPASGKHKAVSTCGSHL
 SIVLLFYGAGLGVYISSVVTDSPRKTAVASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAACCTGCAGCCCGTCTTTTACAGCCTGTTCTGTCCATGTACTGGTCACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCATGTACTTCT
 30 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTTAAGCACAAACCAGTACCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT
 TTGTCTTGTTTTTTGGCTGGCTTGGAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTCACCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGC
 TGATTCTTCTCTCTGTTGACTAGTGTTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTTG
 35 AGGCTGTCCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA
 TCCAACCTACCTGTTTCAGACACCCTCATCAATAACATCCTGATATATTTTGACGCTTGATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTACAGGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

45 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLIILAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMA YDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 50 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHL SVVALFYGTTIGVYLCF
 SSVLTTVKEKASAVMYTAVTPMLNPFYSLRNRLK GALRKL VNRKITSSS (SEQ ID NO: 295)

55 ATGGAACCAAGAAACCAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCATGTACTTCT
 TCCTGGCCAACTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 5 TCCGACTTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCATTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
 10 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH
 15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLLIATSFLAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
 LKLSGSDTHFNIVIMAFSSFIVISCMIVLISYLCIFIAVLKMPISLEGRHKAFTSCASYLMAVTIF
 FGTLFMYLRPTSSYSMEQDKVSVFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

20 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
 CTCCACACCCCCATGTATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 25 TCCGTCACCTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCCTGGGGACTGAGTGCTTCCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
 CATAACATACAGGGATGACTTTTAGGTTGTCCTTTTGTGGTTCTAATAGGATCAACCAATTTCT
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTGCTCTGATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTATTGTATCATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT
 GTGTATCTTCTATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCAACATATTCTTTGGAACAATCCTCTTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
 35 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 TAAAGAAGATCTTATGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSIITKKTFSFNFCRENIIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS
 SYSFDMKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATACAGTGAAGTGTGTTTATACTGCTGGGCTTCACCACAGACCCA
 GGAATGCAGCTGGGCCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGAGTCTTCTTCT
 50 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTCAATCATACCAAGAAAACGTTTTTC
 CTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTTGCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
 55 TGTCATCTGCCCCGAGTGCTCATCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCAC TTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAACTTCTCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIINKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSAKLKLSFHGFNTINHHFCELLSLISLSPDSYL
10 SLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPSASGHRKVFTSCASHLTAITIFHGTLFLYCVF
NSKNSRHTVKVASVFTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

15 ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
ATTACCTGGAAGTCAAATTCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCCATGT
ATTTTTCTCTCAACCACTCTCCTTTGTGGATTCTGCTATTCTCCATCATTTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
CTTTTTCTTTTGCACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTTAATGAGATAAGCACACTACTCATCATTCTGACATCTTATGCATTATCATTTGTCACCA
25 CTTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCTTGTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA
30 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICYVSSSTAPKMLSDIITEQKTSIFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
35 PLYTVLISHTLCLKMVVGAYVGGFLLSSFIETYSVYQHDFCGPYMINHHFFCDLPPVLALSCSDTF
TSEVVTFIVSVVVGIVSVLVVLISYGYIVAAVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVNPPIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

40 ATGGCTGTAGGAAGGAACAACAATTGTGACAAAATTCATTCTCCTGGGACTTTTCAGACC
ATCCTCAAATGAAGATTTTCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
TGGAAGTAAAGCCTCATTGCCCTCATTAAGATGGACTCTCACCTGCACATGCCCATGTACT
TCTTCCTCAGTAACCTGTCCTTCTGGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAACCAATTCCTTTGTTGGCTGTGCCACTCAGTACT
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATAACACTTTGTTTAA
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTCATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTTCTGTGACCTCCCTCCAG
TCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
50 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCCAGCTA
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT
CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
55 AGGGACCCCGGGATTCTCACGGTGGACCATTCAATTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSLVFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
5 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLLPLFCGPNVLDTFYCDVHRVLKLAHTDIFIL
ELLMISNNGLLTTLWFFLLLVSIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP
FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

10 ATGGAGATGGAAAACCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
GGGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTTCTGG
TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
15 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
TGGCCATCTCCAAGCCCCTGCACATGCGACTATCATGAGTAGAGACCATGCAATTGGGCT
CACAGTGGCTGCCTGGTTGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC
CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCTC
CAAACCTGGCCCATACAGACATTTTCTACTTGAACCTACTAATGATTTCCAACAATGGACTG
20 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA
GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT
GGTGACCCTGCATTTCTGTCCTGCATCTATGTCTATGCCCAGGCCCTTCACTGCCCTCCCA
TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
TCTGATAGAAAATAG *SEQ ID NO: 306)

25

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLTTLAWNLAFLIRGDTHLHTPMYFF
LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI
SSPLLPTIMTQGLCTRMVVGAYVGGFLSLIQASSIFRLHFCGPNIIINHFFCDLPPVLALSCSDT
30 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTAL
FVYLRPSSSYLLGRDKVVSFVSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
NO: 307)

35 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCTAAGCAACTTATCTTTCATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC
40 AGTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTGACTGCTATGGCATA
GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGGCGGACCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCCCTGGCTCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCGTG
GTGGTCACTGTGCGAGGAACATCGTTCCTCCAACCTCCTTATCTCCTATGGTTACATAGTGT
45 CTGCGGTCCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTCTGCTGACTTGGCAGCCAG
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTGATTGGTGATCCCC
ATGCTGAACCCTCTCATTTACAGTTTGAAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

50

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCVVFVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVFHFGCTEIFILTVMA YDRYVAICKPLHYM
TIMNRETCKMMLLGTWVGGLHSHIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETIYIG
55 VVV TANS GTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFM YMRPD

TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACAAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTGTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCT1ATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
10 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCCTTTTGTGGACCAATGAGATAGATCACTACTTTTGTGATGTTTACCCTGTGTTGAAA
CTTGCCTGCACAGAAACATAACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
15 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCCACATTGCCATGGTCG
TTATCTTTTTTCGGCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

AOLFR169 sequences:

MMDNHSSATEFHLLGFPQSQGLHHILFAIFFFFYLVTLMGNTVIIIVIVCVDKRLQSPMYFFLSHL
STLEILVTTHVPMMLWGLLFLGCRQYLSLHVSLSNFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI
25 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

30 ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTTGCTATATTCTTTTTCTTCTATTTAGTGACATTAATGGGAAAC
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCCT
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTG
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
35 CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTCACTTTACCTTC
CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCTT
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACTGTGTTGTGATTG
40 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCAAGCAAACACAGGGAGTTGAGTACAA
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTCATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVITFTGCMVQFYFHFSLGSTSFLIL
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
50 FFCDFNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILTCNQTVKTVLQGMQ
RLKGLCKAQ (SEQ ID NO: 313)

55 ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTCAATGGTTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTTCTTGCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 5 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGGCCAGGATGCTCT
 CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGGTGACCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
 15 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMIGGFVHSVVQIVFLYSLP
 ICGPNVIDHSVCDMYPLLELLCLDITYFIGLTVVANGGIICMVIFTFLISCVILNFKTYSQEER
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNFPFDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA
 TGACTTCTTCCTTGCCCTACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCCCTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACACTTACTTGGTGGTGACAGAGGTCTTCCCTTTGGTGGTGATGGCCTA
 30 TGATCGCTATGTGGCTATCTCTAAGCCGCTGCATAATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGCCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT
 CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 35 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
 ACTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATTCTAGTTCTA
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
 45 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
 VELVVGNTQATNLYGLALSIAJSGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

50 ATGGCAGAAACTCTACAACCTCAATTCCACCTTCTACACCCAAACTTCTTCATACTGACTG
 GCTTTCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCCTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCACTTATA
 TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
 5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCCTTG
 GTACATGTAGTTCTCACATCTGTGTCACTTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
 CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC
 AGAGACCGACTCCTGGAAACCTTCACATTAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPGLPGLEAYHIWLSIPLCLIYITAVLGNLSILVIVMERNLHVPMYFFLS
 MLAVMDILLSTTTVPKALAFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC
 APLRYTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITY
 15 NIWYGFSVPVIMVILDVILIAVSYSILRAVFRPLPSQDARHKALSTCGSHLCVILMFYVPSFFTL
 THHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGVAHRFFDIKTWCCTSPPLGS
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTCCTGGCATCCCTGG
 20 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTGCCTCATTTACATCACTGCAGTCC
 TGGGAAACAGCATCCTGATAGTGGTTATTGTATGGAACGTAACCTTCATGTGCCCATGTA
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
 CCCTAGCCATCTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCAAAGGC
 TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
 25 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
 AGGATTGCTCTGGCCGTCATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCCTCACTCCTACTGTGAGCATATTGGA
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTGGGTATGGCTTCTCAGTGCCCAT
 TGTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
 30 TGTTCGTTTGGCCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT
 CTGTGTCTATTATGTTTATGTTCCATCCTTCTTACCTTATTGACCCATCATTTTGGGCG
 TAATATTCTCAACATGTCCATATCTTGCTGGCCAATCTTATGTGGCAGTGCCACCAATGC
 TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
 CTTTGACATCAAGACTTGGTGCTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

AOLFR175 sequences:

MHFLSQNDLNINLPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
 LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
 SGCFLQFYFFFSLGSTECFFLAVMAFDRLAICRPLRYPTIMTRRLCTNLVNCWVLGFIWFLIPI
 40 VNISQMSFCGRSRIIDHFLCDPAPLLTLCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVRAVL
 RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLNPIV
 YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
 45 TCATTAGTAATTGCTGGTGCTTTTACAATTACAGGCACATGAAAATCTTCAACAGCCCC
 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
 AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC
 ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
 ACTTCTCCTTCTTGGAGATATGTTATGTACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
 50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTTCTTCTCC
 TTGGGCTCTACAGAATGCTTTTCTGCGAGTTATGGCATTGATCGATACCTTGCCATCTG
 TCGGCCTCTACGCTATCCAACCATATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
 GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC
 TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
 55 CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
 TCTTCTCTTCATTGTGGGGTCTATGCTCTGGTCGTGAGAGCTGTGTTGAGGGTCCCTTCA

5 CGAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCACCACCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCGTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:

AOLFR176 sequences:

10 MFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGGQREMQSCFFSFILVLYLLTLLGNGAIVC
AVKLDRLRHTPMYILLGNFAFLEIWIYISSTVPMNMLVNILSEIKTISFSGCFLQFYFFFSLGTTTECF
LSVMAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGFLCYPVPIVLISQLPFCGPNIIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFSLILGSYTLVIRAVLCIPSGAGRTRKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSNGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

15 ATGTTCTTTATTATTTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTTCATCTGCTGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGACGTGAAATTGGACAGCGCGCTCCACACACCCATGTACATCCTTCTGGGA
AAGTTGCTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAACATCTAGTCAATAT
20 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTCTTTTTTTC
ACTGGGTACAACAGAGTGTCTTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTCCCT
25 TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATTGTTTGCAGTGGC
CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGTCTGGTCAAACTAAAGCTTTCTCCACATGTGGGTCCCACTAATGGTGGTGTCTC
TATTCTATGGAACCCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

35 MSFFFVDLRPMNRSATHIVTEFILLGFGPCWKIQIFLSLFLVIYVLTLLGNGAIIYAVRCNPLLH
TPMYFLLGNFAFLEIWIYVSSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTTECLFLAVMAYD
RYLAICHPLQYPAIMTVRFGCKLVSFCWLIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRAKAFSTCGSHLVVVSIFYG
TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRIRQNS
(SEQ ID NO: 325)

40 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
AGTTTATTCTCCTGGGATTCCTGGTTGCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
45 ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTTGCTTCTTCTGAGATCTGG
TATGTGTCTCCTCACTATTCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
ATTTTCTGGGTGCTTCTCCTCCAGTTCTATTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCTGTC
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTGG
GATACCAATTCCCATTTTCTACATCTCCCAACTCCCTTCTGTGGTCTTAATATCATTGAT
50 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCAACTG
AATGTATTTTCTATACTCAGAGCTCCCTTGTCTCTTTTCACTAGTATGTACATTCTTCGA
TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAAG
CCTTCTCTACCTGTGGTTCTCATTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
ATGTATGTAAGTCCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT
55 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO: 326)

AOLFR178 sequences:

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
LQYLTIMSPRMCMFFLVAAWVTGLIHSVQLVFVNNLPFCGPNVSDSFYCDLPRFIKLACTDSY
RLEFMVTANS GFISLGSFFILIISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLF FGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGTCAGAGTTTGTGTTCCTGGGACTCACCAATTCCT
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTTGTCTCACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTTCT
GTTAGCCAACTCTCCTTCACTGACCTGGGTGTTTCTCTGTCACTTCTCCAAAATGATTT
15 ATGACCTGTTGAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT
GTGGCCATATGTAAGCCCCCTCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
TCTTAGTGGCTGCCTGGGTGACCGCCTTATCCACTCTGAGTTCAATTGGTTTTGTAGTA
AACTTGCCCTTCTGTGGTCCTAATGTATCGGACAGCTTTTACTGTGACCTTCCTCGGTTTCAT
20 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC
ATCTCTCTGGGCTCCTTCTTCACTGATCATTTCCTATGTGGTCATCATTCTCACTGTTCT
GAAACACTCTTCACTGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCACGTCAGTGTG
GTAGTTTTGTCTTTGGTCCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCCTCACTCCTGTTTTAAATCCTATCATCTACA
25 CATTAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

MNGMNHSSVSEFVFMGLTNSREIQLLLVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
30 LHYLTIMSPRMCLYFLATSSIIGLIHSVLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC
GGGAGATTCAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
AACCTTGTCATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCTT
CCTGGCTAACCTCTCAATCATTGATATGGCATTGCTCAATTACAGCCCCTAAGATGATTT
GTGATATTTTCAAGAAGCACAAAGGCCATCTCCTTTGCGGGATGTATTACTCAGATCTTCTT
TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTGTGGTA
GATTTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
CAGACTTGCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTTACATCTTCACTGTTCACTGTTTG
45 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCATGTC
GTCATCTTGTCTTTGGGCCACTGATGTTTTCTACACATGGCCTTCTCCACATCACACCT
GGATAAATATCTTGCTATTTTGTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
CATTAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
TTACAAAGATTTTGTA (SEQ ID NO: 330)

50

AOLFR180 sequences:

MTNKMAYIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSSNFLLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRLHKKPMYYFLSMLAAVDLCLTITLPTVLGVLFHAREISFKACFIQMF
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
55 HGGHELHSPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR
QAMFQLLQSKGSWGFNVRLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCTCATAGT
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCCTCAAACCTTCC
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTTCATCATTACTAAGCGGA
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
ATTACGACCCCTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCGGGAGATCAGCTTTAA
10 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
ACAGACAGGATGGTCCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
TTCCCCTTCTTGAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGATCAGCAGTTTTT
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCCTAT
GTCCTGATCCTCCGTAAGTGTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA
GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA
TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
GGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

25 MSVLNNSEVKLFLLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYYFLAML
AVSDMGLSLSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
IYGFFIALCTMLDLALIVLSYVLILKILSIASLAERLKAALNTCVSHICAVLTFYVPIITLAAMHFF
AKHKSPLVVILIADMFLVPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
AACATGCCCACATTTGGTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCATCATGTTGA
GGGTCTTCTTGTTCATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATCTTC
35 ATTCATGGATTCACTGTGATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAAATG
GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTACCTTAAGGAG
ATTAAAAATATTGTCAAAAAGATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
AGCTGGCCTGCTCTGACAACAAGACCAATGTCTATGGCTTCTTCATTGCTCTCTGTACT
40 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG
CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
GCCCTCTTGTGTGATCCTTATTGCAGATATGTTCTTGTGGTGGCGCCCTTATGAACCCC
ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

MTLGLSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSLFESSVLLSMAFDRFVAICHP
50 LHYVSILTNTVIGRIGLVSLGRSVALIFPLPMLKRFYPYCGSPVLSHSYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
GTTTTCCATCCCGGGCAACTGCACAATCTTTTTATCATTAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
TCTCCCTACAGTCTGGGCATCTTTTGGGTTGGAGCACGAGAAATTAGCCATGATGCCTGC
TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTCCTCGAGTCCTCTGTGCTACTGTCTATG
5 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAAGTGTAGCACTCATTTTTCCATTA
CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
GTTTGTTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
10 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
TGTTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTTCATCC
ATCGCTTTGGAAGCAGGCACCCACCTGGTCCAGGTGGTTCATGGGTTTCATGTATCTTCT
CTTCTCCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA
GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYYYFL
SILALTDVSLMSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGLVSMADFDRFVAIRN
PLHYVSILTHDVIRKTGISVLTRAVCVFVPVFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR
20 INSLYGLIVIFTLGLDVLLTLLSYVLTLKTVLGVSRGERLKTLSLTHMSTVLLFYVPMGA
ASMIHRFWEHLSPVVHVMADIYLLPPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCCACCGTAACTTCATTCTGACAGGTATCCCAG
GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTCTCTACACACTCACACT
25 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGTATGCATGCATGCAGAT
GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC
AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTG
30 AAAGACTGGAATATCTGTCCTCACCCGGGCAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT
ATAAAGTGCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTACTGTCTTACACAAAA
CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGT
ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTCACCTGAAGAC
TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCTCAGCACATGCCTCTCTCAC
35 ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

AOLFR184 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTPLPIAVYLLSALGNGTILWIALQPALHR
40 PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSLFVVL SAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHL SAVLLF
YIPMILLALINHPITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGGAGQ
(SEQ ID NO: 339)

45 ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC
TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTTGTCTAGTGTGTCTGATATTGGATTGGT
50 CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTGCTGGTGCTCACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTTATCCATGTCTTTTCTGTCTATGGAGTCCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
ATCTGCCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCCATAACCCAT
55 TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTTGTGGTTCTTTTCAGCCATGGGTTTGGACCCCTGCTTATTTTCTTCTCCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
CAAACCTGTGCTGCCCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

AOLFR185 sequences:

MFYPILNDISTKNNNSNIMSCCNILFIKTVEIILVYNQTSPPWYPIVPSKSLVYNNNTCFDCYHLQR
10 VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
MAMALDCYVATCFPLRHSSILTPSVVIKLGTVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCA DTSSIRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPPMLNPIIYGVRTKQIGDRVIQGCCG
15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTATGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTTGATTGTT
20 ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACCAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCCTGCTTGGAATCCCAGGCCTG
GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT
25 GGCCATATTCTGGTTTCATGCTCATGAGATTGAGTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCGTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCTTCTGCTTCATGGTGTC
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
30 CTGAAGTTGGTGTGTGCTGATACAAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
CTGTGGCTGGCTTTGATGATTGTGATTGATGTCATACGTGATGATTTTGAGAGCTGT
GCTTCAGTTGCCCTCAGGTGAAGCCCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTTGTCATCTTGGCTCTTTATATCCAGCCCTTTTCTTCTCCTCACCTACCGCTTGGCCAT
GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
35 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

AOLFR186 sequences:

MSNASLVTAFLTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNL
40 FIDMWFSTVTPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAI
RYTSMMSGSRCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADT
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRRTSDGRRRAFQTCASHCIVVLCFFVPCV
PGSMDAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLKRDKVAHPQRK (SEQ ID NO:
343)

45 ATGTCCAACGCCAGCCTCGTGACAGCATTCTATCCTCACAGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
50 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCTGGGGAGCACCAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTCCAT
TTGCCCTACTGTGGACCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTCTGATAGTGTCTCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGILI
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHLFIHSA
10 VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
ILLFYVPALFSVFAYRFGRSIPCYVHILLASLYVVIPPMNLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
GCAACTACATATCGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAAGTTCTT
CATTCACTTCCTCTTCATTCATCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
25 TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCCTACATCCACATCCTCCAAGCAGTCTTCCGC
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTATTCTCCTATGCTCAAT
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

MFPSLPCPVLLVQLPLMNENMQCFVFCSDSLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
35 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRRLRHLSPPTSEEHMKNKNNVTEFILL
GLTQNPGEQKVLVFTFLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRCVCL
MLLAAWIGGFHLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
AVTFITILLSYGVILHSLKTQSLEGKRKAFYTCASHVTVVILFFVPCIFLYARNSTFPIDKSMTV
40 VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACTTATGAATGAGAACAT
GCAGTGTGTTTGTGTTCTGTTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
45 ATGTCCCATTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAACGTTGGTCGATAAGGCATCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTGTTTGTAGGC
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAAACATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTTATTTGTACATT
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
50 AGCCAGTCCCTGGGTTCCCCCATGTACTTTTTTCTGGCTTCTTTATCATTCATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTCT
55 TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
ACAACTTCTGTGTGATTGTATCCCTTATTGAACTTGCTTGCACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC
 TTTCTATGGGGTCAATACACTCTCTTAAGACTCAGAGTTTGAAGGGAAACGAAAAGC
 TTTCTACACCTGTGCATCCCACGTCACTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
 5 TAATCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

10 MQQNSVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSPPMYFFLFYLSF
 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
 TIMSQVQCHILIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL
 VNSGAICSSSFMIILISYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPMD
 KMOVAVFYTIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
 GGCAGAAAATAGTGTGTTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
 TTTTATTGTCCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
 20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
 CATTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCCTTACCAACCATCATGAGCCAGCAGGTCTGCATCATCTGATT
 GTTCTTGCCTGGATAGGGTCTTTAATACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
 GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTGAAAC
 25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACTGAGAAACC
 ACAGTGCCAAAGGGGAAGAAAAAGGCTCTCTCCGCTTGCACGTCTCACATAATTGTAGTCAT
 CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCGACCACTTTCCCCATGGACA
 30 AGATGGTGGCAGTATTTTATACTATTGGAACACCCCTTCTCAATCCACTCATCTACACATCT
 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:

35 MQRNHTVTEFILLGFTTDPGMQLGLFVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
 LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
 YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPVLKLACSVRESYQ
 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPPSS
 YSLKRDKMVSTFYTMLFPMNLNPMIYSLRSKDKMDALKKFFKSA (SEQ ID NO: 351)

40 ATGCAGAGGAGCAATCACACAGTGAAGTTCATCCTGCTGGGCTTACCACAGATCCAG
 GGATGCAACTGGGCTCTTTGTGGTGTTCTGGGTGTGTAAGTGTGCTGACTGTGGTAGGAAG
 TAGCACCCTCATCGTGTGATCTGTAATGACTCCCGCTACACACACCCATGTATTTGTCA
 TTGGAATCTGTCAATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
 ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAAGTCTTCTCTGC
 45 CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
 ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG
 GATTTTGTGGTGACAATGTCATTGATGACTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
 GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCTTCTGGCCTCCAATGTC
 ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
 50 CCACTTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA
 CCTTATACTATGGCTCCATTCTCTACAACACTACTCCCGGCCAAGTCCAGCTACTCCCTCAAG
 AGGGACAAAATGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
 (SEQ ID NO: 352)

55

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
FIDVCYISSTVPKMLSNLLQEQQTITFVGCIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS
SIMSPTLCVWMLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV
5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
10 TGGAACTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
CTTCCTCAGTAACCTGTCCTTCATAGATGCTGCTATATCAGCTCCACAGTCCCCAAGATGC
TCTCCAACCTCTTACAGGAACAGCAAACCTATCACTTTTGTGGTTGTATTATTCAGTACTTT
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTCACCCACCCCTCTGTGTTTGG
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTTGT
TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAAGTGT
TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCACACCTGTGCTTCTCATCTAAC
20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAGAGA
AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRY AALCKPLHY
TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPLLTLSCSDNYISEM
VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
CTGCAGATCCCCTCTTCATAGTCTTCCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCCTCA
35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
GTTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTTCTTG
TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTACTACTGGGAACACTTTCAGGC
40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTCTGTGATGCTCCTCCTCTCTTGACT
CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG
TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRY AAVCKPLHY
TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
55 357)

ATGGAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCCTCTTTATAACGTTCCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
 GGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
 5 GTAACCTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
 AGCTTTTGCCACTGTGGAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 10 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

20 MERQNQSCVVEFILLGFSNYPELQGQLFVAFLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
 SVVDLSFSAVIMPEMLVVLSTEKTISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVFMKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTFL
 FEIYAFTGTFLIILVPFLLILLSYIRVLFKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLQ
 PKSGYSPETKKVMSLSYLLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO: 359)

25 ATGGAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCCTGGTTATTTATCTGGTGACCCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 30 TTCTCCTGAACCTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 GGTGGTCCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
 TTCATCCTTCTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAAGTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTCACAGGCACCTTTTTG
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTTCAGATTCTGTTTGCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTACAACCCAAATCTGGCTACTC
 ACCGGAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

45 MIVQLICTVCFLAVNTFHVRSSFDLKAADDMEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSVPSTLVSLISKRNISFSGCAVQMFF
 GFAMGSTECLLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLAMRL
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVLPLMVIFFSYMFIYTLQMNSATG
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEELQALDKLISLFYGVVTPMLNPILYSLR
 NKDVKAADVLYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTCAAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTCAGAA
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
 55 CTCATTTTACACACCAATGTACTTCTTCTGGGCAACCTCTCTTTCCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGTCAATGGGGTCAACAGAATGTCTGCT
TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA
5 ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
TCATTTTCGCATGTGAAATATTAGCTGTCCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTTTC
TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
10 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
AAGCTCATTTCTCTGTTTTATGGGGTAGTGACCCCATGCTGAATCCTATACTCTATAGCTT
GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAACCAATTCATA
A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLQIPMYYFLSNL
SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFAFADAECILILAAAMAYDRYAAICNPLL
YTTLMSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDTQINQL
LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
20 YSLDTDKVVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAACCTATGGTCGGA
AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTCAAATTCCCATGTATTATTT
25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
CAAACCTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
CTTCGCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
CATTTGTGTTGGCATATTTCACTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCACCTCTTCT
GGCTTTATCATGTACAGACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG
AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
TAATTTATAGTTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:
364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGVMVRHTNESNLAGFILLGFSDDYPQLQKVLFLVILILYLLTILGNTTI
ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGLVHLYNSHALGS
TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCLMALASMAWLSGIATTLVQSTLTLQLPFCGH
RQVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
45 GTCFSLTLVVTIFYGTIIFMYLQPAKSRSDQGKFSVLFYTVVTRMLNPLIYTLRIKEVKGALKK
VLAKALGVNII (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTCTGATTATCC
50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
CTTTCTCATCTCTCCTTCCCTGTACCGCTGCTTCACCAGCAGTGTTATTTCCCAGCTCCTGGT
AAACCTGTGGGAACCCATGAAAACATATCGCCTATGGTGGCTGTTTGGTTCACCTTTACAAC
TCCCATGCCCTGGGATCCACTGAGTGCCTCTTGGCTCTGATGTCCTGTGACCGCTATGT
55 GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
 AAGCTGGCTTGTGTGGGCACCACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT
 TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTTG
 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTCGGGACCTGCTTCTCCACCTGACA
 5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
 CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
 GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAYDRYAACVCKP
 LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
 TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGHQAALSTCASHFTAVSVFYGTIVIFIYLO
 15 PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
 TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
 GGGATGATGTGTGCTGATCTGATGGACTCTTGTCTCCACACCCCCATGTACTTTTTCTCAG
 20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
 TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCAGATGTTCTTCTTTGT
 AGCCTTGGCCACGGTGGAATAACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
 TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC
 25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
 GTCTTGTCTGTATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
 TTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC
 ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
 CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCCAGCTCCAGCCACTCCATGGAC
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAAT
 TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

MDTGKNTLPQDFLLGFPQSQTLLQSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
 NLSFLEIWYTAAVPAKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLLAAMAYDRCLAICY
 LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
 VELVAFVIAVVVILSSCLITFVSYYIISTILRIPASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
 35 TSIKDALDLIAVHVLNTVTPVLNPFYITLRNKEVRETLLKKWKWK (SEQ ID NO: 369)

ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
 AAACCTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
 AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
 TCTGAGCAACCTCTCCTTCTGGAGATTGGTATACCACAGCAGCAGTGCCCAAGCACTG
 45 GCCATCCTACTGGGGAGAAAGTCAGACCATATCATTTACAAGCTGTCTTTTGAGATGTACT
 TTGTTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
 CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
 TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
 TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
 50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
 GGTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
 TCAGGATCCCCTCTGCCAGTGGCCGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCTTCACGTCCGCACCTCTATCAAAGAT
 GCCTTGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTTAAACC
 55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
 GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVYITLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLOMYFFISLATTECILFGLMAYDRYAAICRPLL
5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIHHFFCDSPPLFKLSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

10 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
TGGAGCTACAGATTATCCTCTTTTGTGTTTTCTTGATTTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
CCTGGCTAACCTGTCTTTGTGGACGTTTGTAACTCAACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTACT
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
15 TGGCAGCCATATGTCGCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTTGTGTCAGGGTGTGTAAGTTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCAATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
TTCAAGCTCTCTTGTGTCGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
TGAATATTGTGGGGACTCTGCTTGTGTCATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
20 TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTTCTTTCTGTGA (SEQ ID NO: 372)

25

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSTIPSTLVSLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN
30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDLDATDKIISMFYGVMTMPMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
373)

35 ATGGAATGGGAAAACCACACCATTTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTAGAAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCTTACCTGTGAAATTCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTCATATTGACACCTTTGTTATTAATCATTTGTCTCTTACACGTTAATCATTTGTGAGCATC
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCTCTACCTGTTTACGCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
GTAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSTIPSTLVSLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN
55 EFILLVTTTLFLLTPLLIIIVSYTLIISIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFYRVMTMPMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATCTGGTGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCCCT
CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
10 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTGAGATGACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTA AACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

20

AOLFR203 sequences:

MKRQNQSCVVEFILLGFSNFPQLQVFLGVFLVIYVVTLMGNAITVIISLNQSLHVP MYLFLLN
LSVVEVSFSAVITPEMLVVLSTEKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLF
25 EIYAFTGTILIVMVPFLILLSYIRVLFKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRITLIKLRWRKVILHTF (SEQ ID NO: 377)

ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG
30 AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGTGATCCTCTTGTCTTACATTGAGTTCTGTTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVWVGFLHATIQLFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSIVILRSLKNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRVSTLPI
50 DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTCCTG
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTCAGCTCCTAAGTTGATTGTGGA
TTCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVFSFGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFTSCSAHLTVVIIIFYGTIFFMYAKP
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDBGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTCTCCTGGTAGGGCTTTCTGCCCACC
CAAAGCTCCAGACAGTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGATTTTCTT
CCTCTGTAATCTTTCTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAAATTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSLHTPMYLFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCQIAAGSWMTGCLTAMVEMMSVLP LSLCGNSIINHFTCEILAILKLVCVDT S
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALSMH
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCTCCTGGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAAC TTTGTTTCAGGGAGAAACACTATTTCAATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCCACCTGA
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFLALILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS
FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY
5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
TLAVSNIAFLVPLLVIFFSYMFILYILRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
CCAAACTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
CCTGGGCAACCTCTCTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCCTTGGCATGATGGCATTGTATCGTTAT
GTGGCCATCTGTAACCCCTTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT
GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
TAAAATTAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
CTTGGGAAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTTCCATGTTTTATGGGGTTGTGA
CCCCCATGTTAAACCCCATATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
25 ATATTTGCTGAGCAGGAAAGCTATTAACAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRRNDTNVADFILTGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL
THLSFIDLSYSTVTPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAAICSP
30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSM SRLHFCD SNIIHHFFCDTSPILALSCTDTDN
TEMLIFIIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTIMIFTYLPK
RKSYS LGRDQVAPVFTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
TTTTCTCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAAC
CTTAGCGAACTTACTGACTTCCAACATATTTCTTACACGGGCTGCTTTGCCCAGATGTTCT
GTTTTGTCTTCTTGGGTA CTGCTGAATGTTATCTTCTCCTCAATGGCCTATGATCGCTAT
40 GCAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGCCCAAAAGGCTCTGCCTCGCTC
TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT
AGCTCTGTCTGCATGACACAGACAACACTGAAATGCTGATATTCATTATCGTGGTTCC
ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
45 GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
GGAGTCACCATCTTCTATGGAACATATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

AOLFR211 sequences:

MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIIRLDLQLHTPMYFFL
THLSFIDLSYSTVTPKTLANLLTSNYISFTGCF AQMFFAFLGTAECYLLSSMAHDRYAAICSP
LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSM SRLHFYDSNVIHHFFCDTSPILALSCTDTYNT
55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLPK
SYS LGRDQVASVFTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

5 ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 10 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAACATATATTTCTTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTGCCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 15 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCTGCACTGATACATAACAACACCGAAATCCTGATATTCATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTACAAATATCTGCATCCTATGTGTTTATTCTCTTTACCATCCTGA
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTTACTTATTTAAACCAAGAAAGTCTTATTCCT
 20 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT
 CATTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFVVLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSVTPKALVNFQSNRRSISFVGCFFVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
 LYSVVMSSQKVSNNWLGVMPIYVIGFTSSLISVWVISSLAFCDSINHFCDTALLALSCVDFTFGT
 EMVSFVLGFTLLSLLIITVYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 25 NTSSLTQAQVASVFYITIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
 30 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCAAGTAGTCATGTCCCAAAAAGTGTCCAACCTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTTCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAGGCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACATCTTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCATTCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDHPR
 EAVLFVFLFFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVSVLVFVIPPALISISYGF
 50 TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

55 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCCTTTTCTTCTACCTCCTGACCTTGTGGGA
 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTT
 TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTTGTGTAGTGTTCTGT
 TTGTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVVIMSRRTCTVLVMISWAVSLVHTLSQLSFTVNLPFCGPNVVDSSFCDLPRVTKLACLDYIIE
 ILIVVNSGILSLSTFSLVSSYIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPVLNPIIYTLNRNRMKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAA ACTCCAGCTTTTCTATTTTGTCTTCTCTGTGTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTTGGGAAACCTTTCCTTTGTTGACATTTGTGAGGCTTCTTTTGCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAAACTTGCCTGCCTGGACTCTTACATCATTTGAAATACTAATTGTGGTCAATAGTGAATT
 CTTTCCCTAAGCACTTTCTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATTCTTTGGACCTTGCATCTTCTATGTGTGGCCCTTACCATCTCTCCTTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCCGTCCTAAACCCCATTTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLHSVSHLAFTVDLPFCGPNEVDSSFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALIISYTIILIGVRCRSSGSSKALSTLTAHITVVILFFGPCIFYIWPFSRL
 45 PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCATTATTTCTTTGACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTTATTGATATCTGTGAGTCTAATTTGCCACCCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCGTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCACTGTGTGAGCCACTTGGCTTTTACAGTG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTCCACATCACAGTG
 GTCATTCTTTCTTCGGGCTTGCAATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL
 10 TNLSIIDMSLASFATPKMITDYLTHGKTISFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPL
 HYASVISPQVCVALVVASWIMGVMHMSMSQVIFALTLPCGPEYVDSFFCDLPVVFQLACVDY
 VLGLFMISTSGHIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIPTPLNPIIYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACCTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTCTCTTTTCGCCACCCCAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTACAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
 ATTGCAATATGCAAGCCCTGCACTATGCTTCTGTCATTAGTCCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCATTCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCCTGTGGTGT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGTCTGTTTATTGTTTATTTAATTCATATGTTATTGTCTGTTACTGTGAA
 GCATCATTCTTCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTCATTGTTG
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEGCMTQMFFLHLLGGAIEVLLISMSFD
 35 RYVAICKPLHYLTMSRRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSFFCDLPVIK
 LACVDYILGVFMISTSGMIALVCFILLVISYIILVTVRQRSSGGSSKALSTCSAHFTVVTLFFGP
 CTFIYVWPFTNFPIDKVL SVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGATTGTTCGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTGACACATATATTC
 50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCCTGGTCACCGTTCCGGCAGCGTTCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCTTTTCTTTGGCCCATGCACTTT
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLTGLSQTREVLVLFVIFLSFYLFILPGNLIICTIRLDPHILTSPMYFLLANLA
LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQLFHLFVGASEMFLLIVMAYDRYAAICRPLHYA
5 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLMFGPSIYIYARFDF
SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
10 GGGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
AATATCCTTATCATTGTCACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTTCTT
GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCATAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
GGTGGCTCTCTCCTGGATGGGGGCTTCATTCACTTCTATAATACAGGTGGCTCTCATTGTT
CGACTTCTTTCTGTGGGCCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG
TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
GATCTCTGTGGTGTGTTTCATTGCTCTGTAAATGTCCTATGCCTTCTTCTGGCCTTGCTCA
20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT
TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATCCCTTTACTTAATCCCAT
ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

AOLFR219 sequences:

MLTSLTDLCFSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF
LIILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN
30 KVDSEFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVNRSSASMAKAR
STLTAHITVVTLFFGPCIFIYVWPFSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS
RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
TGTAATTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
GTGTTGTGCTCGTCCTCATTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
TTCACGTGTTAATCTGCCATTTTGTGGTCTAATAAGGTAGACAGTTTCTGTGACCTTCC
TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT
45 AGTGGCTTTCTTTCTGAGTTCTTTCTCCTCTGGTTGTCTCCTACACTGTAATACTTGT
ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTACGCTTATTTTAAACCCTGT
AATCTACACGCTAAGAAACAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA
50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
(SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMPHAHRGGLLFFIPLLLIYG
55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
HSLGITESCVLTAAMADRYIAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAHLAVFLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCAATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCTCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCTGCTTAATCAGTGAGCAGAAGAGCATTTCGTGGC
TGGCTGCCTCTCGAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCTCTGTG
15 CTTCTGAGATTGCATGGATTTCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATGTAGCCTCCTTCTGGTCAATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT
TGAGATTCTCAGCCACCTACTCAGTGTGTTTGGGACACAGCAATTGCTGTCACTTTTGTTATC
20 CTTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVVEEFVLVGFPPTPPLQLLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTIPRLAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFGFSSMMKLLFISQLSYCGPNINHFFCDISPLLNLTCSDKEQA
ELVDLLALVMILLPLLAVVSSYTAIIAAILRIPTSRGRHKAFSTCAAHLAVVVIYSSTLFTYAR
PRAMYTFNHNKIISVLYTIIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTGCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTT
35 CTTGGCCATCTCTCTTTCCTGGAGCTATGGTACATCAATGTCACCATTCCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACCTGACTTC
TTTATTGCCTGTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTTATTTCCTCAA
40 TTGTCCTACTGTGGACCCAACATTATCAACCACTTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIIIAIRLDSHLHTPMYFLSFL
SFSETCYTLGIIPRMLSLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFGLMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLLVLSFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCCCTTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGGCTGTACTAACTGCTTCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCATTACTTCTTCTGACTGGATACTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCCTCTGCTGAGGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTCATTATGGCTGTGCTTCTTCTGTACCTGAGGCCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSLAGCLTQMYFFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLLRLSC
 SDTHHIQLLIFTEGAAVVVTPFLLILASYGAIAAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSRREAEGWRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCCCACCTGTCTTTGTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCAAGATG
 30 TTGGCCAACCTGTTGGCCCATGACCCTCCATCTCGCTGGCTGGCTGGCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGTAACCTGATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT
 35 CTCTTAAGGCTCTCGTGTCTGTACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCTCGCCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTGATGTACACTGTAGTCACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIIALSWLDLRLHTPMYFFLSHL
 45 LDLCFTTSTVPQLLINLCGVDRITIRGGCVAQLFIYLALGSTECVLLVVMADFDRYA
 AAVCRPLHY MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKL
 ACADTEGT EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTCGSHLLV
 VFVFLFYGSAIYT YLQSIHNYSEREGKFVALFYTHITPILNPLIYTLRNKDKVGALWKVL
 WRGRDSG (SEQ ID NO: 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCACCACCAGCACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGTATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCTGCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG
GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
5 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT
CGTGGCTGTTCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
10 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQTSTDFILLGLFPSSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM
15 SKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
LRSPTEKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTCATCTTATTGGGGCTGTTTCCACCATCAA
20 TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTCATTTTCTGATGGCTCTAATTGGAAACC
TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG
AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTGTTCTTAAGATGGCATCTGA
TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTTCT
TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
25 TATTTGCTTTCCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTA TACTCCATA
TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
CTGGCCTGCATGGACACCTGGGTCTATGAGGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
TCGTGTTTCCCTTCATTGGTATTTTCATGTTCTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
GTAACCTTCTACTATGCACCTTTTGTCTACACTTACTACGTCCAAGATCCCTGCGATCTCC
AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
ANMSFLEIWYVTVTIPKMLAGFVGSQDHDGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
RYMAICYPLHYPVIVSGRLCVQMAAGSWGAGGISMVGVFLISGLSYCGPNIINHFFCDVSPLL
40 NLSCTDMSTAE LDFILAI FILLGPLSVTGASYVAITGAVMHIS SAAGRYKAFSTCASHLT VVVIIF
YAASIFIYARPKALS AFDTNKLVS VLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
KKASRN V (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC
TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCCATGTAC
TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
GCTTGCTGGCTTTGTGGATCCAAACAGGATGATGGACAGCTAATCTCCTTTGAGGGATGC
ATGACACAGCTCTACTTTTCTTGGCTGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT
50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC
GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA
AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTCT
ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLHRGLCARLVVVSCTGVSTGFLHSMMSRLDFCGRNQINHFFCDLPPLMQLSCSRV
YITEVTIFILSIIVLCICFFLTGPIYVFISSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMIV
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTTCTGCTGTTAGGATTCCAGAACCTTC
TTGAATGGCAGGCCCTGCTCTTTGTCATTTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCTCCTA
GCCAACCTGCTGTCTGGGGCCAAAGCCATCTCTTCTGCTGCATGGCACAGCTCTACT
TCTTCGTATTCCTCGGCGCCACCGAGTGCTTTCTGCTGCTTTCATGGCCTATGACCGTTAC
CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTGAGCACAGGCTTTCTGCATTCCATGATGATTTC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCATATT
GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTTELWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHIDSR LHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREIN
HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

35

ATGTTTTATGTAAATCAGATACCTTTTCAACTTTATCATATCTCTTTTCGTGTACCCTACAGA
GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTTCTCTGCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTTCTATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC
CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCGTCACCA
TGCAAGTCCCCTTCTGTGCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCAGCAGACAGCCATGTATGCTCTGTATTATTA
TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCTACTCATTTACAGCCTTAGGAACAAGGATGTCACGGGGGCCCTACAGAAGGTTGTTGGG
AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

55

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLIHPAFPGLLFAIVFSIFVVAITANLVMILLIHMSRLHTPMYFLLS
QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTIGGEFFLLGLMAYDRYVAVCNP
LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHHFCEIPAVLKLSDTDS
5 LYETLMYACCVLMMLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSIFYGAIFY
TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR
KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCTGCTGGGCTGTGCAGTTCAGATCTT
CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC
15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
CATGGTGGTCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
ATGAGTTTCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
GCTGAAGTTGTCTTGCACAGACACGTCACCTCTATGAGACCCTGATGTATGCCTGCTGCGTG
CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT
20 CCACAGGATGAACTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
ACACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCCATGCTCAA
CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
GAGATGTGGTTCTCCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
25 NO: 430).

AOLFR231 sequences:

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSLHHTPMYFLLSNL
SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMADRYVAICKP
30 LHYMTIMSPRVLTGLLLSSYAVGVFVHSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
LQLLVIADSGLLSLVCFLLLLVSYGVIIFSVRYRAASRSSKAFSTLSAHITVVTLFFAPCVFIYVW
PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCACTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
35 AAAATCTTCAGATTTTATTCTTCTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
AACCTGCTCATCTTGGTGACTGTGACCTTTGATTTCGCTCCTTCACACACCAATGTATTTTCT
GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG
TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCCAGATGTTCTT
TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCCACGGGTGCTCACTGGGC
TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG
ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCTTGTGAT
TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
CTGTCACTGGTCTGCTTCTCCTCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
GATAAAATTCTTCTGTGTTTACACAATTTTACACCTCTCTTAAATCCTATTATTTATAC
ATTAAGAAATCAAGAGGTAAAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:
432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVNKNIS
APECGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
55 GFTFTPTMTFPRGSREIHHFCEVPAVLNLSGSDTSLYEIFMYLCCVLMMLIPVVISSYLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTILTPVVPN
LIYSLRNKDVMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTCAATGGGTGTGAATAA
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTCTCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCCTCATGAACCATAGGGTGTGTCTCTTCTGTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA
AAAAGGCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTAAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFILMGLFRRSKHPALLSVVIFVFLKALSGNAVLILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMMLIPVTIISSSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACTGTGACGCCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTCAATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCCGGAATTTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTCTCCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA
TGCTGTGTCCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAAGGCCTTTGCCACCTGCTC
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDRYVAVCQPL
HYPVIVNSRICIQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLKLSCSDTFSNE
VMIVVSALGVGGGCFIFIIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRPP
AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCTATTATTTA
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGATECILLVMAFDYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
 LLPAKNSKQDQGFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGCTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTTCATTCCCTGTTCTACTCGTTGGTACACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAIHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLIRTAQGRQRAFPCTAQLTGVLVYVPPVCIYLQPRSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLLCSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

5 CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTCCGCCTGCTCTACT
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCTAAAGCTCGCCTGT
 ACAGACACCACCATTAAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 10 GCCTCATCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTCCGAGAGTCTACAG
 15 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

15 MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRIYAISKPL
 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCGPVLDTFYCDVPQVLKLACTDTFT
 LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIYVYA
 RPFTALPTDTAISVTFTVISPLLNIYTLRNQEMKLMRKLKRRLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
 AAACTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCTCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCCTGGGTGGGGGGCTTGTCCTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACACTGGGGAAGGAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACC
 TGGTGACCTGCATTTTCGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCC
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

40 MAPENFTRVTEFILTGVSSCPQLIPLFLVFLVLYVLTLMAGNLGIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 LLYMVVVSRRLLCLLVSLTYLYGFSTAIVSPCIFSVSYCSSNIINHFCIDIAPLLALSCSDTYIPE
 TIVFISAATNLFSSMITVLVSYFNIVLSILRIRSPEGRKKAFSTCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDLDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCAATGCCCCATAAATGCTG
 ATGAACTTTTAGTAAAGAAGAAAACCTACCTCATTCTATGAATGTGCCACCCAACCTGGGAG
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
 TCTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGTCTGATACTTACATAACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTCCACCTGCGCTTCGCATATGATA

CGAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSQKLISFGGCAQIFFLHFTGGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASWVGVFVHSISQVAFVNLPCGPNEVDSFFCDLPLVIKLACM
10 DTYVLGIHMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTGAGAATTTGTGTTGCATGGACTCTGCACTTCAC
GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
CCTGTGGGGAACCTAGCTTTCCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
ATCAGGGATTTCTTAGTGATCAAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAACTCT
TCTTCTTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCTTGCATTACATGACTTTGATGAGTTGGCAGACTTGCATC
20 AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
GTGATCAAACCTTGCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTTGTTTATGTGCGGCCTTTCAGTAGGTTT
TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTACTCCACTCCTGAACCCCATAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAQMYVFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSFFGTASITYIRPQ
35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACTTGTCTGGG
40 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCT
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCCACGGGCTGCTT
GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
45 ATCTTCTCTTACCTTTTCGACGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATCCCCCTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGCAGGCA
50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55 MPQILIFTYLNMFYFFPLQILAENLTMVTEFLLLGSSSLGEIQLALFVVFLFLYLVLSGNVTIIS
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYITVTPLLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTCTGTATCTAGTCATTCTTAGTGGCAA
TGTCACCATTATCAGTGTTCATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCAATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG
CCATTTGTCACCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC
TTGTGGTTCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTTATTATGGCTGTGCTTCTTCTATCTACCTGAGGCCTACAGCAAACCTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTTGGGCAAGAAA
GGTTCTCTAAAACCTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLIGIPGLESMLHWVGPFPAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIPLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGARLSCASIRVNIYIG
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHFRGR
NIPHFHILLANFYVVIPALNSVIYGVRTKQIRAQVLKMFENK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTTCTGGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTACAGCTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG
GCCATTCTGTCTATCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCTATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAGTTATGGCA
CTGGCCATCTTTCTGAGACCCCTAGTCTTTGTGCATACCCCTTGTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC
40 CTGTCTTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTCCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTACAGCACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTCTCATTATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAAGTGCTGAAAATGTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNKTVVREFVVLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLSQHSFG
SQLVIFMLGVFALVIPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSCASFIYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTGCTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCAATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCCAGAAGAAGACCATTTCCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGTCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCATTCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCCGTTGGAAGATAACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAAGTGTTCAGTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATACACTTC
 AAGCCAAGACACCCTAATATCTGTGTACATACACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

MWQEYYFLNVFFPLLKVCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
 MGLFNRKETSGLIFAIHSIIFFTALMANGVMIFLIQTDRLHTPMYFLLSHLSLIDMMYISTIVPKM
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLSRRVCWMI
 20 IAGSWFGGSLDGLLTPITMSFPFCNSREINHFFCEAPVLKLACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

25

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT
 ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTACTTCTCTCAGCCACCTTTCCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCCTCTG
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCTCTGAGATACCTGTCC
 TCATGAGCCCGCGGTCTGTTGGATGATTATAGCAGGTTCTGTTTGGGGGCTCTTTGGA
 TGGCTTCTCTTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAAAC
 35 ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTCTCTGTAGTCCTTGCTT
 CCTATGCCCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTCTGTGTTTT
 40 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCCTCAAAGGGTGTGAGGAGGTGT
 CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

45 MDLKNGLVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP
 LHRYTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE
 LFVIADSGLLSFTCFILLVSYIVILVSPVKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFS
 ASNKTALVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
 GGGAACTTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCTTCATTCTCCCTTGACTTTCT
 CCTTGGAATCTCTCTTTTTTGGACATGTGTCTCTCACTGCCACAACACCCAAGATGATCA
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTTTACACTCCATAAGCCAGATAGTTTAAACAAT
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCTTGTGA
 TCAAGCTTGCTTGCATTGAAACATACACCCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTACCTGTTTCATCCTCTTGCTTGTCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
 GTCATCTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTAGTAGTTTGGCAAG
 CAATAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQA VFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 LALTDISFSSVTVPKMLMDMRTKYKSILYECCISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRSLFCAANTIPHVFCDLAALLKLSCSDIFLNE
 LVMFTVGVVVITLPFMCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVSVSLYYGSIFGQYLF
 PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTACACCCCCATGTACTTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 25 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
 AGTGGCTGTATCTTGGAATCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGTGCCCCTGCTC
 AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTTCATGTGTATCCTGGTATCATATGGGCTACATTGGGGCCACCCTCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
 35 CAACATTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVIYELITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPILL
 40 YYVIMSQRLLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFTSTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC
 45 CTGAGCTGCAGATTTCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTATTATGCATGTGCTGCACAGCTGGCATTCT
 TTCCTTATGTTTCATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT
 50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
 TGGGCATTCAATATCTCTACAGCACATTTAGGCTCTGATGTTCACTATTAAGATTTTTACA
 TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTTGACAGTGG
 TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL
ATECVLLATMSYDRIAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHAVVSLFYGSIIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCTCTCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACCTCCCCTTCTGGACATGAGCTTCACCACGAGCATTGTCCCACAGCTCCTG
GCTAACCTCTGGGGACACAGAAAACCATAGCTATGGAGGGTGTGGTCCAGTTCTAT
ATCTCCCATTGGCTGGGGGCAACCGAGTGTGTCTGTGCTGGCCACCATGTCCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCTATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTTGCAGATGCCCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGCTTTTGTGTCTCTGCCTCTGGGGCTCATCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIIVLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHILAFVDICYTSAITPKMLQSFTEN
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDFLMFTELVIIFSIIYIM
VTILKMSSTAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGA CTTAAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTGCGAGGAAACAGCACTGAAGTGA CTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTCA GCATGTCCTTTTCA TTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTC
CACAACATTTGGCTTTTGTGTATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGGGGCTGTGTGATACAATTCCTAGTTT
ATGCAACATTTGCAACCACTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTCTTGC
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG
ATGCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCCTCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
DMGLTSSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
5 MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVVGKAFSTCSSHLVCVVFYGTLSAYLC
PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAACCAATCCAGCATTCTGAATTTTCTCCTCCGAGGAATATCAGCGCCTCCAGAGC
AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
10 CTCATCATCCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
CAACCTGTCTTTTGTGACATGGGTTTAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
ATACAGACTCGGCATCACACCATCTCCTATACGGGTGCCTCACGCAAAATGTATTTCTTTCT
GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
15 ATTGTGCTGGGTCTCACCAATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
CCTTCTGTGTGACTGGGGAATTTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
TCGTCCCCTTTTATGCATTGTACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
20 GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG
AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALAILLCGLFSAFYTLTLLGNGVIFGIICLDCKLHTPMYFFLSHLA
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHPLRY
NILMSWRVCTVLAVASWVFSLLALVPLVLILRPFCEPHNHFCEILSVLKLACADTWNQV
VIFAACVFILVGPLCLVLVSYLRILAILRIQSGEGRRKAFSTCSSHLVCVGLFFGSAIVTYMAPK
30 SRHPPEEQQKVLISLFLNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCCAAGATGCTGACG
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGCTCTGG
CTGTGGCTTCTTGGGTGTTTCAGCTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG
40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTCAGCCTGCGTGTTCATCCTG
GTGGGGCCACTCTGCCTGGTGTCTCTACTTGCATCCTGGCCGCCATCTTGAGGA
TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
TATATAGCCTAAGGAATGCAGAGGTCAAGGGGCCCTGAGGAGGGCACTGAGGAAGGAG
AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
IDLTYISVTPKMLVNQLAKDKTISVLGCGTQMYFYLLGGAECCLLAAMAYDRYVAICHPLR
YSVLSHRVCLLASGCWFVGSVDGFMLTPIAMSFPFCRSHEIQHFFCEVPAVLKLSGSDTSLY
KIFMYLCCVIMLLIPVTVISVYYYIILTIHKMNSVEGRKKAFTTCSHITVVSFLFYGAAIYNYML
PSSYQTPEKDMSSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGA CTTTTCCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCTGGCCGCCTCTGCTTATCTTCAGTATATTTTGTATGGCTGTGTCTTGG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGTCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCATCCTCACCATCC
 ATAAGATGAACTCAGTTGAGGGTCGAAAAAAGGCCTTCACCACCTGCTCCTCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACCTACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTTACAGTTTCAAGGAATAAGGATGTCACAAGGGCTTTGAAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

20 MTFFSSGGNCEPVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 ILLIHSEPR LHTPMYFFISQLALMDLMLCVTPKMLVGQVTGDDTISPSCGCIQMFFHLTLAG
 AEVFLLAAMAYDRYAAVCRPLHYPLLMNQRCVQLLSACWVLGMVDGLLLTPITMSFPFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRKA
 LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPLNPLIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCTTTCTTGTATGGCCCTCACTGGGAATGCCC
 TCCTCATCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCCATGTACTTCTTCATCAGC
 30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATACCATTTCCCGCTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCTTGGCTGGAGCTGAGGTTTCTCCTGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
 35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCCATCATGGTCATCTCCAGCTCATAACCCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGCCGGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCCATGATCATAGTG
 CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGGAGTTCTACACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 MDTLFICTTVPKLLADMVSKEKHSFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNVPCGSR SINHFFCEIPAVLKLACADTSLYET
 LMYICCVLMLLIPISIISTSYSLILLTIHRMPSAEGRKKAFTTCSHLTVVSIFYGAAFYTYVLPQS
 50 FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACCSSAQKVATSDA (SEQ ID NO:
 477).

55 ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT
 CATGATATTCTTGATTGAGGTGGACTCTCGCCTCCACACCCCCATGTACTTTCTGCTCAGTC
 AGCTGTCCATCATGGACACCCTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAACCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
 5 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
 GGCCTGTGCAGACACGTCCTTGATGAAACTCTGATGTACATCTGCTGTGTCCTCATGTTG
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTCCTCCCACTTGACTGTAGTT
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
 AGCAGGACAAAGTAGTGTACGCCTTCTATACCATTGTCACGCCCATGCTTAATCCTCTCAT
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

15 MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSRHTPMYFLLSQLS
 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMSRKICWLIVAAAWLGGSIDGFLLPVTMQFPFCASREINHFFCEVPALLKLSCDTDSAY
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCTCCACACCCCCCATGTACTTCTC
 25 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG
 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCCTCCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCCTCATGAGCCGCAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT
 GCAGTTCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
 GATGTCCTCATCCCTTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
 ATAGGATGAGCGAGGCGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
 TGGTTGTGAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
 ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
 GGTGTGTGTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

40 MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLGNGVIFGHIICLDSKLHTPMYFFLSHL
 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF
 QYTVIMSWRVCTILASTCWISFLMALVHITHILRPPFCGPQKINHFICQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPVMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGAATCTTCTCTGTCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
 50 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
 TATTTGGCTTTTGTGCTGTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
 55 GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGGCCATCTT

5 GAGGATCCAGTAATGGGGAGGGCCGACACCGACTTACTCTTCCTGCTCCTTCCACCTTT
GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCTGAAAAGAGTGTTGTGG
AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

10 MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPMKLANLVMHKKVISFAPCILQTFLYLAFAITECLILVMMCYDRYVAICHPL
QYTLIMNWRVCTVLA STCWIFSLLALVHITLILRPF CGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAGS AFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

15 ATGGAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
GCTCTGGAGTTGTTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAACTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTG CATACTT CAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCAACCCCTTGAATACACCCCTATTATGAACTGGAGAGTGTGCACTGTCCT
GGCCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTTATTTGCGGGTTCTGCGTTCA
TCTTAGTG GGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGT CATGTACATGGCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

30

AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNP LLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

40 ATGGGGGACAACCAATCACGGGTACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTG CATTATGCAGATGGCTTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTGT
45 GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTTCTGTCTGCCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTCGGGCCCCCTTTCTTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTINKTISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
5 IYGLMVISYIIVDVILIASSYVLILRAVFLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCCTTCTTCCTCCTGCTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTCTTTTCCCATTTCTGTATTGTGTACCTGATTGCCATTG
10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCTGCAACCCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT
TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT
20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTCTTTTATGACACATCGTTTTGGCCAA
AACATTCCTCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCCACCTGCCCT
TAACCCTGTCATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNIILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP
LRYSMILTINKVAILGIVHVRTLVFVTPFTFLTLRLPFCGVRIIPHTYCEHMGAKLACASINVIY
GLIAFSVGYIDISVIGFSYVQILRAVFHLPAPWDARLKAALSTCGSHVCVMLAFYLPALFSFMTHRF
30 GHNIPHYIHILLANLYVVVPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCTCGTAGTGGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGCTACAGCAACCATCCCCA
AGATGCTGGGAATTTTCTGGTTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
GATGTATACCATTATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
40 TAGCCATTCTGGGCATAGTCATCATTTGTCAGGACTTTGGTATTTGTGACTCCATTACATTT
CTCACCTGAGATTGCCTTTCTGTGGTGTCGGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTCATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
45 GTTATGTTGGCTTTTCTACCTGCCAGCCCTCTTTTCTTCATGACACACCGCTTTGGCCACAA
CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
ACCCTAAAAGCTTTTGGCATTGTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA
ATAA (SEQ ID NO: 490)

50

AOLFR112B sequences:

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSHLQTPMYFFLRNFSF
LEISFTNIFIPRVLISITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
MSSRICIQLIFCSWLGLMAIPTITLMSQQDFCASRNLNHYFCDYEPLLELSCSDTSLIEKVVFL
55 VASVTLVVTLLVLVILSYAFIHKILKLPAAQQRKAFSTCSSHMIVISLSYGSCMFMYNPSAKEG
DTFNKGVALLITSVAPLLNPFYITLRNQQVKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTTCCTTGGCTATTTACTCAGCATCCTTGGAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTCTCCG
 5 GAACTTCTCCTTCTTGGAATTTCTTTCACAAACATCTTCATTCCAAGGTCCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCATTATCAAGACTATTCTGAAG
 CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT
 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
 TTACACCCTAAGGAACCAACAGGTAACAACCCCTTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNVPMQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHLPFCGNNQINYFFCDIPLLILSCGDTSLNE
 LALLSIGILISWTPFLCIILSYLIISTILRISSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISSYS
 LEKDRLISVLYSVVTPMLNPVIYTLRNDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTCACCATCTTCTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 30 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG
 CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTCTTCTGTGACATACTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAAGTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTCTGTGCATCATCCTTTCCTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCCCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTACACCCATGCTGAATCCT
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFLSIYLFVVGNLGLILLIRADTSLNTPM
 YFFLSNLAFFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
 VAICNPLLYMVVMTPGICQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL
 TCSDTRFKQLWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIINKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTTCTGTTACTCTTCTGTCATT
 55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
 CTACTIONACTGGGCTGCTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
 5 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 GCCTGTGCTGGTATCATGTTTCATTTCCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTACAGTCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 10 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNITIPFHACATQLGCFLTFMITECFLLASMAIDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINFYCDLPLALSCSDTHMK
 EILIFAFAGTDMISSSSIVLTSYIFIIAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTATGTCACTGTATTTCATTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAACGCAACACCATTCCCTTCCATGCTTGTGCAACCCAACCTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTTCATTGTGATGACCTCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCTTTGCTGGCTTT
 30 GATATGATCTCTTCCCTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACAAAGCCATTTCACCTGTGGTCCCATATGGTGA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGATAAAG
 35 GTTGTGAAAACCTTACAGATATTAACATTTTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTIITLTLDDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRLTSMITTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI
 LLAVVTLMVTLVLVTLSTYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
 GGA FNKGIAVLITSVTPLNPFYITLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCCCTACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG
 GAATTTCTCCTTCTTAGAAATTTCCCTTCACATCCATTTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
 CTGCTCCTGGTTGGGGGGATTCCCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCTCCACATGATTGTCTATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL
CVHLVVASVISGLFSLQLVAFISLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
AIAVPPFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

10

ATGGAATTTGTGTTCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGCCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTGAT
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTGCCCACCCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
TGTTCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCAGAACAGCTAG
(SEQ ID NO: 502)

20

25

30

AOLFR276B sequences:

MGGFGTNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIIKEEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
LRYATVLT DVRVAHNGISIVIRSF CMVFPLPFLKRLPFCKASVVL AHSYCLHADLIRLPWGD
TINS MYGLFIVISAFGVDSL LILLSYVLILHSVLAIASRGERLKT LNTCVSHIYAVLIFYVPMVSVS
MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

35

ATGGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCTT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGACCAGCCAATG
TACTACTTCTGTCTCTTTTCTGTTAATGACCTGGGTGTGTCCTTTTCTACATTGCCCACT
GTACTGGCTGCTGTGTGTTTTCATGCCCCAGAGACAACCTTTTGATGCCTGCCTGGCCCAGA
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCACAATGGCATATCCATTGTCATCCGCACTTCTGCATGGTATTCCCACTTCCCTTCCTC
CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG
CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTAT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
ACATATCTATGCAGTGTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTTCATCGAT
TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

40

45

50

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINF SANLGMIVLIRMDYQLHTPMYFFLS
HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDYKAINP
LLYTVNMSSRVCYLLLTVGYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

55

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHSAEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGTCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGATGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTTCAAGAGTTTTTCAATTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTCTTTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTTGGTTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAGTAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVDFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIIEFLFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIALCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACA
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
30 AAATGTGTCTATCCTTGTTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTCT
TCCTGGGAAACTTGCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGTCCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATTCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTCGTACAACTGAGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA
MLDSIDLSLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIAVLRSLYMPIVLVLLRLPFCGHRHPIPTYCEHMGARLACASIKVNIM
FGLGSISLLLDVLLILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATACTTCTTCATTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTTCCAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
 GCCTCATTGCAGGCATTGCTGTCTGAGGAGCTTGACATGGTCATTCCACTGGTGTCTTCT
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
 5 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
 CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
 GATATTCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCTCCCACCCT
 10 CAATCCTGTAATCTATGGGGTCAGAACCAAACATATTAGGGAGACAGTGCTGAGGATTTTC
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVVTAGTEACLLSGMAYDRHAAIRRP
 LLYGQIMGKQLYMHVWGSWGLGFLDALINVLLAVNMVFCFAKIIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTTGGGCTGTCTGCCGACC
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTTACCTCCTGACCATAATGGA
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG
 GAGAACCTCCTGTCACAGAGGAAAACCATTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
 25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
 TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
 CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
 TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
 CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTTGTCTGCTCCACTCTCC
 30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCCACTCA
 CTGCAGTGACACTTACTATGGCTCAGGTTTGCTCCGCCATCTCATGCCAAACTCAGGTTT
 CCCCATAGAGTTGATCTTCTCTGTGCACTACTGTAGTCACTCCCATGCTGAATTCCTCA
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGAAAAAATATT
 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)